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                       GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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        mycoplasma

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        Q59745
        rhizobium 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KIFVAGHRGLVGSAİVRKLQEQGFTNLVLKTHABLDLTRQADVESFFSQEKPVYVILAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                            member of the short-chain dehydrogenase/reductase family that catalyzes two distinct reactions at the same active site."; Structure 6:1601-612(1998).

-!- FUNCTION: TWO STEP NADP-DEPENDENT CONVERSION OF GDP-4-DEHYDRO-6-DEOXY-D-MANNOSE TO GDP-FUCOSE.
                                                                                                                                                                                                                                                                  Somers W.S., Stahl M.L., Sullivan F.X.; "GDP-fucose synthetase from Escherichia coli: structure of a unique
                                  gene in the colanic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipopolysaccharide biosynthesis; Isomerase; Oxidoreductase; NADP;
Multifunctional enzyme; 3D-structure; Complete proteome.
CONFLICT 255 256 EL -> DV (IN REF. 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97077193D79684C7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.4e-72;
56; Mismatches 67
Andrianopoulos K., Wang L., Reeves P.R.;
"Identification of the fucose synthetase
cluster of Escherichia coli K-12.";
J. Bacteriol. 180:998-1001(1998).
                                                                                                                                                                   RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                   MEDLINE=99081889; PubMed=9862812;
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PDB; 1BSV; 26-AUG-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 57.69
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - 1 - SUBUNIT: HOMODIMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 AA;
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   STAND DE REPRESENTATION OF THE PROPERTY OF THE
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RESULT 2. Y4AF_RHISN

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQEVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 IELAHIVCRVVGFKGDIVFDTSKPDGTPRKLLSSERLVSMGWRPKTSLELGLAKSYESFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KIFVAGHRGLVGSAIVRKLOEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.COLI YEFB AND TO MOUSE
                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                              Plasmid sym pNGR234a.
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae: Rhizobium.
                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Preiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: PUTATIVE NUCLEOTIDE SUGAR EPIMERASE/DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.7%; Score 917.5; DB 1; Length 314; 58.0%; Pred. No. 2.2e-70; ive 53; Mismatches 74; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO NODULATION PROTEIN NOLK, E.COLI YEFB AN P35B, M.TUBERCULOSIS RV1512 AND Y.ENTEROCOLITICA WECJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Nodulation; Plasmid; NAD.
SEQUENCE 314 AA; 34674 MW; 2E571D298AA98110 CRC64;
                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                           01-NOV-1997 (Rel. 35, Last sequence
15-JUN-2002 (Rel. 41, Last annotati
Hypothetical 34.7 kDa protein Y4AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000064; AAB91603.1; -.
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                                                                                                                                     (strain NGR234)
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(Rel. 35, (Rel. 35, (Rel. 41,
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(Rel. 39,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOLK AZOCA
P33217;
01-FEB-1994
30-MAY-2000
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYBHGVKKLLFLGSSCIYPKFAPQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 IPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SAKIFVAGHRGLVGSAIVRKLQEQGF----TNLVLKTHAELDLTRQADVESFFSQEKPVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBDINIT: HOMODIMER (BY SIMILARITY).
MISCELLANEOUS: MUTAGEN TREATMENT OF PRIS TUMOR CELLS. PRODUCES TUM-
VARIANTS THAT ELICIT A CYTOLYTIC T LYMPHOCYTE RESPONSE (CTL). THE
ANTIGENIC ALLELE DIFFERS FROM THE NORMAL ALLELE BY A SINGLE
MUTATION IN POSITION 139.
SIMILARITY: BELONGS TO THE FUCOSE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 VIHLAAMVGGLFRNIKYNLDFWRKNVHINDNVLHSAFEVGARKVVSCLSTCIFPDKTTYP
                                                                                                                                                                                                Szikora J.-P., van Pel A., Brichard V., Andre M., van Baren N., Henry P., de Plaen E., Boon T.; Brichard V., Andre M., van Baren N., "Structure of the gene of tun- transplantation antigen P35B: presence of a point mutation in the antigenic allele."; EMBO J. 9:1041-1050(1990).
                                                                                                                                                                                                                                                                                                                                                    De Plaen E.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TWO STEP NADP-DEPENDENT CONVERSION OF GDP-4-DEHYDRO-6-
BEOXY-D-MANNOSE TO GAB-FUCOSE, INVOLVING AN EPIMERASE AND A
REDUCTASE REACTION (BY SIMILARITY).
                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalyia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mush. TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isomerase; Oxidoreductase; NADP; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35877 MW; 358D86D68F173531 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDP-fucose;
GDP-fucose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S -> N (IN TUM- ALLELE)
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Pred. No. 5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDP-mannose to
GDP-mannose to
                                                                                                                                            AND VARIANT ASN-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; M30128; AAA39674.1; ALT_FRAME
$12516; $12516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X53620; CAB94217.1; ALT SEQ. EMBL; X53621; CAB94217.1; JOINED.
                                                                                                                                                                                      MEDLINE=90214611; PubMed=2108859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAB94217.1; JOINED.
CAB94217.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAB94217.1; JOINED
                                                                                                                           SEQUENCE FROM N.A., AND VALLES SEQUENCE FROM N.A., AND VALLES COLLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED
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36.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAB94217.1;
CAB94217.1;
reductase (EC 1.-.-.)].
ISTA3 OR TSTAP35B OR P35B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:98857; Tstap35b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor antigen; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X53623;
EMBL; X53624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X53627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X53622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X53626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X53625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X53628;
                                                                                                                                                                                                                                                                                                                                  REVISIONS
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  83
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                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVIL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGVVGGIHANIADPIHFLADNAAMALNVVMSSFRSEVVTLINLSSSCMYPACIEGPLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALLTASLEPTNEWYALAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGL-EHVNIGSGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAIIEKIHKASQCGSESVSIWGDGTARREFMPAYDFAKIIIKALEVPELIPSSMNVGVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVITIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDILRGPFEVTNEGYALAKTVGLKICEYIDKLPNFNYKTLIACNLYGVGDNFDPRRSHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(GDP-fucose synthetase (FX protein) (Red cell NADP(H)-binding protein)
(Transplantation antigen P35B) (Tum-P35B antigen) (Includes: GDP-mannose-4-keto-6-D epimerase (EC 5.1.3.-); GDP-4-keto-6-L-galactose
                                                                                                                                                                                                                          Holsters M.;
"Identification of a new inducible nodulation gene in Azorhizobium
                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                       Goethals K., Mergaert P., Gao M., Geelen D., van Montagu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.0%; Score 510; DB 1; Length 312; 35.2%; Pred. No. 6.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD/NADP (POTENTIAL).
BC2FCB01C87C097C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S51942; AAB24744.1; ALT_INIT.
                                                                       Hyphomicrobium group; Azorhizobium, NCBI_TaxID=7;
                                                                                                                                                                                   MEDLINE=93113009; PubMed=1472718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.2%
Matches 107; Conservative
                                       Azorhizobium caulinodans.
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  Nodulation protein nolK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 312 AA;
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DWYL 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nodulation; NAD
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P23591;
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Best Local
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126 IDETMIHNGPPHSSNFGYSYAKRMIDVQNRAYFQQHGCTFTAVIPTNVFGPYDNFNIEDG 185
                                                                                                                HVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHV--NI
                                                                                             GSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLAS----LGWTPKVSL
                                                                                                                                                                                                                                                                                          013630; Q9UDG7;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
GDP-fucose synthetase (FX protein) (Red cell NADP(H)-binding protein)
[Includes: GDP-mannose-4-keto-6-D epimerase (EC 5.1.3.-); GDP-4-keto-6-L-galactose reductase (EC 1...-)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDP-4-DEHYDRO-6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dinuclectide phosphate (NADP[H]) binding protein FX: identification with the mouse tum-transplantation antigen P35B."; Blood 85:264-267(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Camardella L., Carratore V., Ciardiello A., Damonte G., Benatti U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REDUCTASE REACTION.
--- PATHWAY: Conversion of GDP-mannose to GDP-fucose; second step.
--- PATHWAY: Conversion of GDP-mannose to GDP-fucose; third (last)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: TWO STEP NADP-DEPENDENT CONVERSION OF GDP-4-DEHYDR DEOXY-D-MANNOSE TO GDP-FUCOSE, INVOLVING AN EPIMERASE AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Primary structure of human erythrocyte nicotinamide adenine
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER.
-!- SIMILARITY: BELONGS TO THE FUCOSE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97066899; PubMed=8910301;
Tonetti M., Sturla L., Bisso A., Benatti U., De Flora "Synthesis of GDP-L-fucose by the human FX protein.";
J. Biol. Chem. 271:27274-27279(1996).
                                                                                                                                                                                                                                                                              321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT TISSUE=Placenta;
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Erythrocyte;
MEDLINE=95102076; PubMed=7803801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC001941; AAH01941.1; -.
Genew; HGNC:12390; TSTA3.
                                                                                                                                                              295 RDGLSQTYDWYLKN 308
                                                                                                                                                                                            302 KOAVKETCTWFTDN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U58766; AAC50786.1;
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:1
MIM; 137020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flora A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLAS----LGWTPKVSL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEEDEVGIKEAAEAVVEAMDFHGEVTFDTTKSDGQFKKTASNSKLRTYLPDFRFTP---F 301
                                                                                                                                                                                                                                                                                                                                                       66 VIHLAAMVGGLFRNIKYNLDFWRKNVHMNDNVLHSAFEVGARKVVSCLSTCIFPDKTTYP
                                                                                                                                                                                                                                                                       7 SMRILVTGGSGLVGKAI-QKVVADGAGLPGEDWVFVSSKDADLTDTAQTRALFEKVQPTH
                                                                                                                                                                                                                                                                                                                           VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
                                                                                                                                                                                                                                                                                                                                                                                                                             121 IPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 HVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHV--NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 HVLPGLIHKVHLAKSSGS-ALTVWGTGNPRRQFIYSLDLAQLFIWVLREYNEVEPIILSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=86808087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FltzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                           SAKIFVAGHRGLVGSAIVRKLQEQGF----TNLVLKTHAELDLTRQADVESFFSQEKPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Galactowaldenase) (UDP-
                                                                                                                                                                          Gaps
                                                                                                                                                                          15;
                                                                                                                      ; Score 463.5; DB 1; Length 321; Pred. No. 6.1e-32; 64; Mismatches 124; Indels 15.
Isomerase, Oxidoreductase, NADP, Multifunctional enzyme. NP BIND 9 39 NADP (POTENTIAL) CONFLICT 5 CONFLICT 5 C -> E (IN REF 3) SEQUENCE 321 AA, 35892 MW, 94BBIFF61658007C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Galactose metabolism; third step. SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcalea; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 273:1058-1073(1996).
-i- CATALYTIC ACTIVITY: UDP-glucose = UDP-galactose.
-i- COFACTOR: NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
11-Lative UNP-Glucose 4-epimerase (EC 5.1.3.2)
galactose 4-epimerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                    28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 KQAVKETCAWFTDN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDGLSQTYDWYLKN 308
                                                                                                                                                                       Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
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Matches
  SSSEE # # # $ 8
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                                                                                                                                                                                                                                                                                                                                                                                                       10;
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s its content is in no way
Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 FFSQEKPVYVILAAAKVGGIHA--NNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SCIYPKFAPQPIPESALLTASLEPTNEW--YAIAKIAGIKTCQAYRIQHGWDAISGMPT 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 IFVAGHRGLVGSAIVRKLQEQGFTNLVLK------THAELDLTRQADVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 GGAVYGEPNYLPVDEN------HPINPLSPYGLSKYVGEEYIKLYNRLYGIEYAILRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDRYSGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 INWKN--BIVNIGTGKETSVNELFDIIKHEIGFRGEAIYDKPREGEVYRIYLDIKKAESL
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIANE=95050273; PubMed=7961465;
Lin W.S., Cunneen T., Lee C.Y.;
"Sequence analysis and molecular characterization of genes required
for the biosynthesis of type 1 capsular polysaccharide in
                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.";
J. Bacteriol. 176:7005-7016(1994).
-!- FUNCTION: REQUIRED FOR THE BIOSYNTHESIS OF TYPE 1 CAPSULAR POLYSACCHARIDE.
                                                                                                                                                                                                             Hypothetical protein; Isomerase; NAD; Galactose metabolism;
                                                                                                                                                                                                                                                                                                                                                   Length 305
                                                                                                                                                                                                                                                                                                                                                                      24.2%; Pred. No. 6./e-14,
ive 72; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                           2756773CF95D50BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                15.2%; Score 250; DB 1; 24.2%; Pred. No. 6.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                  NAD (POTENTIAL)
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entities requires a license agreement (or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || |:: |::|: | GWKPEIDLKEGIKRVVNWMKNN 302
                                                                                                                                                      InterPro; IPR001509; Epimerase_Dh.
                                                                                                                                                                                                                                                                                           34542 MW;
                                                                                                                                                                                 Pfam; PF01370; Epimerase; 1.
                                                                             EMBL; U67477; AAB98196.1; -.
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 24.29 es 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                      HSSP; P09147; 1XEL.
TIGR; MJ0211; -.
                                                                                                                                                                                                                                                                                           305 AA;
                                                                                                                                                                                                                                         Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1280;
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  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 YSHLYNLPTTGLRFFTVYGPWG--RPDMA-----LFKFTKAIVND-QAIDVYNHGNWMR 215
                                                                                                                                                                                                                                                                                                                                                                                                    62 ENYDDLSKVFVDEQPEVVVNLAAQ-AGVRYSIENPRIYIDSNIVGFMNILECSRHFNIQN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 DFTYVDDIVEAISRLVKKPASPNKEWSGADPDPGSSYAPYKVYNIGNNSPVRLMEFVEAI 275
                                                                                                                                                                                                                                                                                                                                                                          44 TRQADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLFLGSSCIYPKFAPQP-----IPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LIYASSSSVYGANTSKPFSTSDNIDHPLSLYAATKKSNELMA--------HT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFLHVDDLADACVFLLDR-------YGGLEHVNIGSGQEVTIRELAELV 253
                                                                                                                                                                                                                                                                                                                    WDAISGMPT----NLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLR
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Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: UDP-glucose = UDP-galactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 KEVVGFEGKLGWDCTKPDGTPRKLMDSSKL-ASLGWTPKVSLRDGLSQTYDWYLK 307
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
UDP-glucose 4 epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-
                                                                                                                                                                                                        Length 334;
                                                                                                                                                                                               13.7%; Score 220,
21.4%; Pred. No. 8.1e-12;
tive 71; Mismatches 128; Indels
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STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
BEDLINE=20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M. Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID≈86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the alkaliphilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: Galactose metabolism; third step.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.
                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                          7 KIFVAGHRGLVGSAIVRKLQEQG------FTNLVLK--
                                                                                                                                                                 2FDFBF8D4D7796CF
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entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                   InterPro, IPR001509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
                                                                                                                                                                 334 AA; 37931 MW;
                                                            EMBL; U10927; AAA64648.1; -.
                                                                                                                                                                                                                                                 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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GALE OR BH1108.
                                                                                                                                                                                                                              Similarity
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                                                                                    HSSP; P27830;
                                                                                                                                              Lyase; NAD.
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Q9KDV3;
                                                                                                                                                                 SEQUENCE
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Matches
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                                                                                                                                                                                                                                                             THSIDTVIHFAANSLVG---ESVKQPIEYYENNVIGTHTLLKKMLEHDVKKIVFSSTAAT 119
                                                                                                                                                                                                                                                                                                                                          218
                                                                                                                                                                                                                                                                                                                 YGEPVQIPIQES----DPTIPTNP-YGETKLAIEKMFHWCQEAYGLQYVCLRYFNAAGAD 174
                                                                                                                                                                                                                                                                                                                                                                                                    ||:|
|LANA-----HYLACEHLRKDGQSGSFNLGNGKGFSVKEVIEVCRQVTGHPIPAEI---A 278
                                                                                                                                                                                                                                                                                                                                                                                       LADACVFLLDRYSGLEHV-----NIGSGQEVTIRELAELVKEVVG--FEGKLGWDC 267
                                                                                                                                                                                                                          62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SERRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mouyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                               YPKFAPOPIPESALLTASLEPTNEWYAIAKIAGIKT---CQ-AYRIQH----GWDAISGM
                                                                                                                                                                                                                                                                                                                                        PINLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWG-----TGSPLREFLHVDD
                                                                                                                                                                                                                                                                                                                                                       -DLTRQADVESFFS
                                                                                                                                                                                                                                             55 QEKPVYVILAAAK--VGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCI
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reeves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                         67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.K., Reeve
                                                                                                                                                     Length 334;
                                                                                                                                                                            Indels
                                                                                                        Complete proteome.
                                                                                                                             2CDFA3DE7336EC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  TKPDGTPRKLMDSSKLAS--LGWTPKV-SLRDGLSQTYDWY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRRSGDPASLIASSEKAQTILGWEPKYPSLETMVEHAWNWH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91260454; PubMed=1710759;
Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana
Structure and sequence of the rfb (O antigen) gene
Salmonella serovar typhimurium (strain LT2).";
Mol. Microbiol. 5:695-713(1991).
                                                                                                                                                                                                8 IFVAGHRGLVGSAIVRKLQEQGFTNLVL----KTHAEL---
                                                                                                                                                    ; Score 219.5; DB 1;
; Pred. No. 2.9e-11;
57; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JULCOSE 4,6-dehydratase (EC 4.2.1.46).
RFBB OR STM2097.
                                                                                         TIGRFAMS; TIGRO1179; galE; 1.
ISOMETASES; NAD; GalactCOSE metabolism; Comple
NP BIND 2
SEGUENCE 334 AA; 37077 MM; 2CDFA3DE7336E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AA
            or send an email to license@isb-sib.ch)
                                                     InterPro; IPR001509; Epimerase Dh. InterPro; IPR000205; NAD_binding.
                                EMBL; AP001510; BAB04827.1; -.
                                                                                                                                                    13.3%;
                                                                              Pfam; PF01370; Epimerase; 1.
                                                                                                                                                  Query Match
Best Local Similarity 27.0%;
Matches 92; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFH-PENSHVLPALMRRFHE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 PSSPYSASKASSDHLVRAWRRTYGLPTIVTNCSNNYGP---YHFPEK--LIPLVILNALE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 AKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQE----VT 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 IRELA-ELVKEVVGPEGKLGWDCTKPDGTPRKLMDSSKLA-SLGWTPKVSLRDGLSQTYD 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 -----QIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESALLTASLEPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                          PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS. SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE DEHYDRATASE SUBFAMILY.
     -!- CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-glucose + H(2)O.
-!- COFACTOR: NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 361;
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P13226;
01-30A-1990 (Rel. 13, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
10D-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase)
GALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.0%; Score 214; DB 1; L 22.7%; Pred. No. 9.3e-11; ive 58; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE008792; AAL21001.1; -. PIR; S15299; S15299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X56793; CAA40115.1;
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413:852-856(2001)
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tes 83; Conserv
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286 AVLVASAGTAREKLGWNPSRADLAIVSDAWEWH 318
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HSSP; P27830; 1BXK.
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nes 89; · Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose + H(2)0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                              Shigella flexneri
                                                                                                                                                                                                                                                              NCBI_TaxID=623;
                                                                                                                                                                                                                                                   Shigella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 CIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGKYLVTGGAGYVGSVVAQHLVEAGNEVVVLHNLSTGFRAGVPAGASFYRGDIRDQDFMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 SFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATYGEPEQVPIVES ----APTRPTNP-YGASKLAVDHMITGEAAAHGLGAVSVPYFNVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 PNDN---FHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSP-----LREFLHVDDLADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANRGVRLVHDPESHLIPLVL---QVAQGRREAISVYGDDYPTPDTCVRDYIHVADLAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 CVFLLDRYSGLEHV--NIGSGQEVTIRELAELVKEVVG-----FEGKLGWDCTKPDGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HILAVRRREPGNEHLICNLGNGNGFSVREVVETVRRVTGHPIPEIMAPRRGRD-----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Gaps
                                                                                                                                                                                                                                                                                             -i- PATHWAY: Galactose metabolism; third step.
-i- SUBUNIT: HOWODIMER (BY SIMILARITY)
-i- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.
-i- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 41
TO 64, 178 TO 184, 218 TO 243 AND 317 TO 329 DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRGVRLV -> YGEYGER (IN REF. 1).
TCVRDYIHVADLAEAHLLAVRRRPGN ->
RPVCATTSTSFPWAPPTCWPCAAARG (IN REF. 1).
WHSSHPKGYDDRG -> LPQRRAGQ (IN REF. 1).
7E520CB140EA9A21 CRC64;
              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                   SEQUENCE FROM N.A.

BEDLINES-88086869; PubMed=3335481;
Adams C.W., Fornwald J.A., Schmidt F.J., Rosenberg M., Brawner M.!

"Gene organization and structure of the Streptomyces lividans gal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGVPAGASFYRGDIRDQDFMRKVF -> EVCRRVPRSSRRHPGRRQV (IN REF. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 1.5e-10;
53; Mismatches 149; Indels
                                                                                                                                                                                                                             Gibson T.J.;
Unpublished observations (MAR-1995).
-!- CATALYTIC ACTIVITY: UDP-glucose = UDP-galactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 RKLMDSSKLA--SLGWTPKVSLRDGLSQTYDWY 305
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                                                                                                                                                                                                            IDENTIFICATION OF PROBABLE FRAMESHIFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01370; Epimerase; 1.
TIGRFAMs; TIGR01179; galE; 1.
Isomerase; NAD; Galactose metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001509; Epimerase_Dh.
                                                                                                                                                                         Bacteriol. 170:203-212(1988).
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    I - COFACTOR: NAD.

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                                                 NCBI_TaxID=1916;
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218
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Sercitype 2A;
MREDINE-94224146; PubMed=8170390;
Macpherson D.F., Manning P.A., Morona R.;
"Characterization of the dTDP-rhamnose biosynthetic genes encoded in the rfb locus of Shigella flexueri";";
Mol. Microbiol. 11:281-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of the rhamnose biosynthetic operon of Shigella flexmeri 2a and role of lipopolysaccharide in virulence.";
J. Bacteriol. 176:3362-2373(1994)
J. CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
-i- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE DEHYDRATASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=YSH6200 / Serotype 2A;
MEDLINE=94209238; PubMed=8157605;
Rajakumar K., Jost B.H., Sasakawa C., Okada N., Yoshikawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR01509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
ILGRPAMs; TIGR01181; dTDP_Gluc_dehyt; 1.
ILIPOPOJYSaccharide biosynthesis; Lyase; NAD.
NP_BIND
NP_BIND
A4 L -> P (IN REF. 1).
CONFLICT 70 76 AQQQDA -> RTAPARR (IN REF. CONFLICT 151 151 A -> T (IN REF. 1).
CONFLICT 160 164 AYAPS -> TKRQN (IN REF. 1).
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CB880B2FF899F909 CRC64;
RFBB SHIFL STANDARD; PRT; 361 AA. P3777; 054162. STANDARD; PRT; 261 AA. O1-0771; 0541621. 30, Created) O1-077-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) dTDP-glucose 4,6-dehydratase (RC 4.2.1.46).
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CONFLICT
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NDEKKKSFRFHHISTDEVYGDLPHPDEANNNEALPLFTTTAYAPSSPYSASKASSDHLV 178
                                                                                                                                                    209 PLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQE-----VTIRELA-ELVKEVVGFE 260
                                        EHGVKKLLFLGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQAY--RIQ
                                                                                                                       RAWKRTYGLPTIVINCSNNYGP---YHFPEK--LIPLVILNALEGKA----LPIYGKGD
                                                                                                                                                                    HGWDAISGMPT-----NLYGPNDNFH-PENSHVLPALMRRFHEAKVNGAEEVVVWGTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94292435; PubMed=7517391; Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M., Stevenson G., Neal B., Liu D., Reves P.R.; Redmond J.W., Lindquist L., Reeves P.R.; "Structure of the O antigen of Escherichia coli K-12 and the sequence of its rfb gene cluster."; J. Bacteriol. 176:4144-4156 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MGIG55,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makin T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Mada C., Yamamoto Y., Horiuchi T., Takedo J., Takemoto K., Mada C., Yamamoto Y., Horiuchi T., Takeo J., Takemoto K., Mada C., Yamamoto J., Horiuchi T., Takeo J., Jakenone G., Manamoto J., Horiuchi T., Mako-Bonding to the Bscherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
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-!- COFACTOR: NAD.
                                                                                                                                                                                                         261 GKLGWDCTKPDGTPRKLMDSSKLA-SLGWTPKVSLRDGLSQTYDWYLKN 308
                                                                                                                                                                                                                           289 EQITYVADRPGHDRRYAIDADKISRELGWKPQETFESGIRKTVEWYLAN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                      RBB1 ECOLI STANDARD; PRT; 361 AA. B37759; P78082; 01-0CT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) dTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
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STRAIN=K12 / WG1;
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                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 SDKKNSFRFHHISTDEVY---GDLPHPDEVNNTEELPLFTETTAYAPSSPYSASKASSDH 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 IQHGWDAISGMPT-----NLYGPNDNFH-PENSHVLPALMRRFHEAKVNGAEEVVVWGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVRAWKRTYGLPTIVTNCSNNYGP---YHFPEK--LIPLVILNALEGKA-----LPIYGK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQE-----VTIRELA-ELVKEVVG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 GDQIRDWLYVEDHARALYIVVTEGKAGETYNIGGHNEKKNIDVVLTICDLLDEIVPKEKS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 APAMARIFAQHQPDAVMHLAAB-SHVDRSITGPAAFIETNI-VGTYVLLBARNYWSALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KILVIGGAGFIGSAVVRHIINNIQDSVVNVDKLIYAGNRESLADVSDSERYVFEHADICD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 ----ESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                             BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY, DTDP-GLUCOSE
DEHYDRATASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
TIGRFAMS; TIGR01181; dTDP_gluc_dehyt; 1.
Lipppolysaccharide biosynthesis; Lyase; NAD; Complete proteome.
NP_BIND
7 13 NAD (POTENTIAL).
PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN
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); Mismatches 139; Indels
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G -> V (IN REF. 1).
C3F64643271C14C7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U09876; AAB88398.1; -.
EMBL; AE000294; AAC75102.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 32, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, D90841; BAA15883.1; -.
EMBL, D90842; BAA15895.1; -.
HSSP, P27830; 1BXK.
EcoGene; EG12412; rfbB.
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Best Local Similarity
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15-JUN-2002 (
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Lyase; NAD.
NP BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 GVKKLLF----LGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQ 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ILVTGGSGFIGSALIRYIINHTQDFVINIDKLTYAANQSALREVENNPRYVFEKVDICDL 63
                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 NVIENIFEKYQPDAVMHLAAE-SHVDRSISGAADFVQTNIVGTYTLLEVAKNYMHTLDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68; Gaps
                                                                                                                                                                                                                           -i- PATHWAY: INVOLVED IN THE SYNTHESIS OF ENTEROBACTERIAL COMMON ANTIGEN (ECA) AND REQUIRED FOR SYNTHESIS OF LIPOPOLYSACCHARIDE O-SIDE CHAINS (EY SIMILARITY).

-i-SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DIDP-GLUCOSE DEHYDRATASE SUBFAMILY.
          Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Marrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirlay R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Pine L.D., Fritchman M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGKLGWDCTKPDGTPRKLMDSSKL-ASLGWTPKVSLRDGLSQTYDWYLKN 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 338;
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66; Mismatches 132; Indels
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SEQUENCE 338 AA; 38329 MW; B44BCC29D6C7D04B CRC64;
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Pfam; PF01370; Epimerase; 1
TIGREAMS; TIGR01181; dTDP_gluc_dehyt; 1.
Lipopolysaccharide biosynthesis; Lyase; NAD;
NP_BIND
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 MEDLINE=95350630; PubMed=7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32769; AAC22531.1; -.
                                                                                                                                                                     Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Conservative
                                                                                                                                                                                                 glucose + H(2)O.
-!- COFACTOR: NAD.
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Matches 84; Conserv
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                                                                                                                              Venter J.C.;
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341 AA.

STANDARD;

ACBB ACTS5 Q9ZAE8;

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RESULT 14 ACBB ACTS5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 EHGVKKLLFLGSSCIYPKFAPQPIPESALLTAS-----LEPTNEWYAIAKIAGIKTCQA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KILVTGGAĞFIĞSHFVTSLISGDIATPQPVTQVTVVDKLGYGGNLRNLABASADPRFSFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 --DLTRQADVESFPSQEKPVYVILAAAKVGGIHANNTYPAD--FIGVNLQIQTNVIHSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 RHHIGRFLHVSTDEVY-----GSIDTGSWAEGHPLAP-NSPYAASKAGSDLLALA
                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KIFVAGHRGLVGSAIVRKL-----OBOGFTNLV-----LKTHAEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucose + H(2)O.
-!--COPACTOR: NAD (By similarity).
-!- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE
DEHYDRATASE SUBFAMILY.
                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Micromonosporineae; Micromonosporaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                     MEDLINE-99214159; PubMed=10196166;
Stratmann A., Mahmud T., Lee S., Distler J., Floss H.G.
Piepersberg W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75AD65EBF737A862 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 DGTPRKLMDSSKLA-SLGWTPKVSLRDGLSQTYDWYLKN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.5%; Score 206; DB 1; 25.1%; Pred. No. 4.1e-10;
                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAD (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF01370; Epimerase, 1.
TIGRFAMs; TIGR01181; dTDP_gluc_dehyt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001509; Epimerase_Dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 NA
37034 MW;
(Rel. 41, Created)
(Rel. 41, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y18523; CAA77209.1; -. HSSP; P27830; 1BXK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                               NCBI_TaxID=1871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | : : : | | | : : | | 1.20 DEKKKNFRFHHISTDEVYGDL-PHPDEVNSNETLQLFTETTAYAPSSPYSASKASSDHLV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FESQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSA---YEHGV- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AEGDGLYFGQHQLDAVMHLAAE-SHVDRSITGPAAFIETNI-VGTYVLLEAARNYWSGLD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 --KKLLF----LGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 HGWDAISGMPT----NLYGPNDNFH-PENSHVLPALMRRFHEAKVNGAEEVVVWGTGS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 PLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQE-----VTIRELA-ELVKEVVGFE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 QIRDWLYVEDHARALYTVVTEGKAGETYNIGGHNEKKNIDVVFTICDLLDEIVPKEKSYR 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KILVTGGAGFIGSAVVRHIINNTQDSVVNVDKLTYAGNLESLAEISDSERYSFENADICD 61
                                                                                                                                                                                                                                                                                 XX MEDLINE-96032389; PubMed-7559340;
XX MEDLINE-96032389; PubMed-7559340;
XA Marolda C.L., Valvano M.A.;
And Arolda C.L., Valvano M.A.;
T "Genetic analysis of the dTDP-rhamnose biosynthesis region of the tentional homologs of rfbB and rfbA in the rff cluster and correct the functional homologs of rfbB and rfbA in the rff cluster and correct location of the rffE gene.";

I Deacteriol. 177:5539-5546 (1995).

- CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-glucose + H(2)0.

- COPACTOR: NAD.

- PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN BIOSYNTHESIS.

- BATHWAY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE DEHYDRATASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 KIEVAGHRGLVGSAIVRKLQEQGFTNLV------LKTHAELDLTRQADVES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.4%; Score 204; DB 1; Length 361;
Best Local Similarity 24.9%; Pred. No. 6.5e-10;
Matches 87; Conservative 62; Mismatches 140; Indels 60; Gaps
                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 GKLGWDCTKPDGTPRKLMDSSKLA-SLGWTPKVSLRDGLSQTYDWYLKN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF12532;
AACG3612.1;
HSSP, P27830; 1BKK.
INCEPPO; IPR001509; Epimerase Dh.
Ffam; PF01370; Epimerase; 1.
TIGRFAMS; TIGR01181; dTDP_gluc_dehyt; 1.
Lipopolysaccharide biosynthesis; Lyase; NAD.
NP_BIND

A. 13
NAD (POTENTIAL).
NP_BIND

A. 10641 MW; 97340068640E57C0 CRC64;
                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-MAY-2000 (Rel. 39, Last annotation update)
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
                      361 AA
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                      PRT;
                      STANDARD;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                               NCBI_TaxID=562;
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289 EQITYVADRPGHDRRYALDADKISRELGWKPQETFESGIRKTVEWYLAN 337

Search completed: June 3, 2003, 05:03:09 Job time: 22 secs

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Sequence 2, Application US/09318271A

Patent No. US20020012979A1

GENERAL INCOMMATION:

APPLICANT: Berry, Alan

APPLICANT: Running, Jeffrey A.

APPLICANT: Running, Jeffrey A.

APPLICANT: Burlingame, Richard P.

TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"

FILE REFERENCE: 3161-24

CURRENT APPLICATION NUMBER: 06/125,073

EARLIER PILING DATE: 1999-05-25

EARLIER PILING DATE: 1999-03-17

EARLIER PILING DATE: 1999-03-18

EARLIER PILING DATE: 1999-03-18

EARLIER FILING DATE: 1998-06-08

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 IPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPE-S 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSDKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
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Pred. No. 5.9e-142;
1; Mismatches 5;
US-10-230-163-240
US-10-140-002-260
US-10-218-631-240
US-10-23-262-260
US-10-123-262-260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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US-09-318-271-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 92.5%;
Matches 298; Conservative
 RESULT 1
US-09-318-271-2
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Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Appl
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Appli
Sequence 148, App
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                3, 2003, 05:04:31 ; Search time 531 Seconds
    (without alignments)
    59.476 Million cell updates/sec
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                                                                                                                                                                                                               1 MSDKSAKIFVAGHRGLVGSA......SLRDGLSQTYDWYLKNVCNR 312
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Sequence 26
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-734-569-148

US-09-734-569-16

US-09-734-569-16

US-09-738-271-6

US-09-738-271-6

US-10-168-066-7

US-10-168-066-7

US-10-121-049-260

US-10-121-049-260

US-10-175-74-260

US-10-175-74-260

US-10-175-74-260

US-10-176-918-260

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-140-474-260
US-10-142-431-260
US-10-143-114-260
                                                                                                                                                                                                                                                                                                 383519 segs, 101223694 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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1646
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Maximum DB
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Thu Jun

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APPLICANT: Running Jeffrey A.
APPLICANT: Running Jeffrey A.
APPLICANT: Buxlingame, Richard K.
APPLICANT: Buxlingame, Richard P.
TITLE CANT: Buxlingame, Richard P.
TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"
FILE REPERENCE: 3161-24
CURRENT APPLICATION NUMBER: 60/318,271A
CURRENT APPLICATION NUMBER: 60/125,073
EARLIER APPLICATION NUMBER: 60/125,073
EARLIER PILING DATE: 1999-03-17
EARLIER PILING DATE: 1999-03-18
EARLIER PILING DATE: 1999-03-18
EARLIER PILING DATE: 1999-03-18
EARLIER PILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 KVGGIHANNIYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADAC------VFLLDRYSGLEHVN 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 KVGGIVANNTYPADFIYQNMMIESNIIHAAHQNDVNKLLFLGSSCIYPKLAKQPMAESEL
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56.9%; Pred. No. 1.1e
tive 58; Mismatches
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Patent No. US20020064816A1
GENERAL INFORMATION:
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Frank, Markus
Freund, Annette
Duwenig, Elke
Schmidt, Ralf-Michael
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APPLICANT: Renz, Andreas
APPLICANT: Ehrhardt, Thomas
APPLICANT: Reindl, Andreas
APPLICANT: Cirpus, Petra
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Best Local Similarity 56.99
Matches 177; Conservative
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APPLICANT:
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TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
TITLE OF INVENTION: in the synthesis of carbohydrates
FILE REPERENCE: BASF-NAB-132-99-US
CURRENT APPLICATION NUMBER: US/09/734,569
FRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: US 60/171,101
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                                                                                                           292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQ 242
PLR-EFLHVDDLADACVFLLDRYS 231
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                       -GLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTP
                                                                                                         233 RGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTP
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SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
HVLPALMRRFHEAKVNGAEEVVVWGTGS
                                                                                                                                              KVSLRDGLSQTYDWYLKNVCNR 312
                                                                                                                                                                   KVSLRDGLSQTYDWYLKNVCNR 314
                                                                                                                                                                                                                                                                           Sequence 148, Application US/09734569
Patent No. US20020064816A1
GENERAL INFORMATION:
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Schmidt, Ralf-Michael
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US-09-734-569-148
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APPLICANT: Bischoff, Friedrich
APPLICANT: Frank, Markus
APPLICANT: Freund, Annette
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APPLICANT: Renz, Andreas
APPLICANT: Ehrhardt, Thomas
APPLICANT: Reindl, Andreas
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Best Local Similarity
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KWYCEN 307
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APPLICANT:
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APPLICANT:
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GPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDR 229
      126 IDETMIHNGPPHNSNFGYSYAKRMIDVQNRAYFQQYGCTFTAVIPTNVFGPHDNFNIEDG 185
                                                                                                                                   GSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLAS----LGWTPKVSL 294
                                                                                                                                                            24S GEEDEVSIKEAAEAVVEAMDFHGEVTFDTTKSDGQFKKTASNSKLRTYLPDFRFTP---F 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VTGGAGFIGSHLVDLLIKEGHEVVVIDNLSRGRLENLSDAEATGKLTFVEADLL-DVDFN
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                                                 HVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHV -- NI
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CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PELICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-7
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
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Publication No. US20020197605A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                      295 RDGLSQTYDWYLKN 308
                                                                                                                                                                                                                                                            302 KQAVKETCAWFTDN 315
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 249-125
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Best Local Similarity
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; ORGANISM: Coryr
US-09-738-626-3862
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TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates FILE REPERENCE: BASF-NAE-133-299-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR APPLICATION NUMBER: US 60/171,101 NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09318271A

Patent No. US20020012979A1

GENERAL INFORMATION:

APPLICANT: Berry, Alan

APPLICANT: Severson, David K.

APPLICANT: Burlingame, Withard P.

TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"

FILLS REFRENCE: 3161-24

CURRENT PLING DATE: 1999-05-25

EARLIER APPLICATION NUMBER: 60/125,073

EARLIER PLING DATE: 1999-03-17

EARLIER PLING DATE: 1999-03-18

EARLIER PLING DATE: 1999-03-18

EARLIER PLING DATE: 1999-03-18

EARLIER PLING DATE: 1999-03-18

EARLIER PLING DATE: 1998-06-08

NUMBER OF SEQ ID DATE: 1998-06-08

NUMBER OF SEQ ID DATE: 1998-06-08

NUMBER OF SEQ ID DATE: 1998-06-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FREFLHVDDLAEATVFLLQNYSAHEHVNMGSGSEVSIKELAEMVKEVVGFQGQLTWDTSK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 LREFLHVDDLADACVFLLDRYSGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGWDCTK 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 SAKIFVAGHRGLVGSAIVRKLQEQGF----TNLVLKTHAELDLTRQADVESFFSQEKPVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QAYRLQYNFDAISGMPTNLYGPHDNFHPENSHVLPALIRRFHEAKVNGAKEVVVWGSGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 VIHLAAMVGGLFRNIKYNLDFWRKNVHMNDNVLHSAFEVGARKVVSCLSTCIFPDKTTYP
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDWYLKN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                               Score 671; DB 10;
Pred. No. 1.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.2%; Score 463.5; DB 35.4%; Pred. No. 1e-37;
                                                                                                                                                                                                                                                                                                                                                                       25; Mismatches
                                                                                                                                                                                                                                                              ORGANISM: Physcomitrella patens
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 74.8%;
Matches 119; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.4%
Matches 111; Conservative
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                                                                                                                                                                                             SEQ ID NO 16
LENGTH: 162
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Gerritsen, Mary E.
               Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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FILE REFERENCE:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 -----VESFFSQEKPVYVILAAAKVGGIHANNTY--PADFIGVNLQIQTNVIHSAYEHGV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 KKLLFLGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 SGMPTNLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLAD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 ACVFLLDRYSGLEHVNIGSGQEVTI----RELAELVKEVVG---FEGKLGWDCTKPDGTP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QAD- 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 374;
                                                                                                                Query Match 14.3%; Score 236; DB 9; Length 37 Best Local Similarity 24.6%; Pred. No. 4.7e-15; Matches 83; Conservative 68; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc_feature
) OTHER INFORMATION: Incyte ID No. US20030087268A1 2801723
US-10-168-066-7
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285 AKEVLGWEPEVNIEQGVAKTVEYF 308
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US-10-028-072-260
Sequence 260, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                         US-10-168-066-7; Sequence 7, Application US/10168066; Publication No. US20030087268A1
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 374
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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/056914
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PELICATION NUMBER: 60/059184
PRIOR PELICATION NUMBER: 60/059263
PRIOR PELICATION NUMBER: 60/059263
PRIOR PELICATION NUMBER: 60/059263
PRIOR PELICATION NUMBER: 60/05260
PRIOR PELICATION NUMBER: 60/052814
PRIOR PELICATION NUMBER: 60/05281
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PRIOR PELICATION NUMBER: 60/06382
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PRIOR PELICATION NUMBER: 60/06373
PRIOR PELICATION NUMBER: 60
                                 Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                 Watanabe, Colin K
Wood, William
Sherwood, Steven
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APPLICATION DATE: 1998-05-0,
APPLICATION NUMBER: 60/084637
                                                             APPLICATION NUMBER: 60/065846
FILING DATE: 1997-11-17
APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/081229
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/066453
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APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/069212
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APPLICATION NUMBER: 60/077791
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-05-13
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FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/0
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83 LSEKDRKRILITGGAĞFVGSHLTDKLAMDGHEVTVVDNFFTGRKRNVEHWIGHENFELIN 142 143 HDVVEPLYIEVDQIYHLASPAS------PPNYMYNPIKTLKTNTIGTLNMLGLAKR 192 300 QYVSDLVNGLVALMNS-NVSSPVNLGNPEEHTILEFAQLIKNLVGSGSEIQFLSEAQDDP 358 ----LLFLGSSCIYPKFAPQPIPESALLTASLEP--TNEWYAIAKIAGIKTCQAYRIQHG 158 WDAISGMPTNLYGP----NDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLREF 46 QADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQ-IQTNVIHSAYEHGVKK-Gaps 214 LHVDDLADACVFLLDRYSGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGW----**.** 99 Length 420; 266 DCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDWYLKNV 309 Indels 138; 1 MSDKSAK-IFVAGHRGLVGSAIVRKLQEQGFINLVLKT Query Match 13.1%; Score 215; DB 9; Best Local Similarity 25.3%; Pred. No. 6.6e-13; Matches 87; Conservative 53; Mismatches 138 R APPLICATION NUMBER: 60/085704 R FILING DATE: 1998-05-15 R APPLICATION NUMBER: 60/086414 R FILING DATE: 1998-05-22 R FILING DATE: 1998-05-22 R FILING DATE: 1998-06-22 R FILING DATE: 1998-06-22 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088730
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088741 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/08858 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090445 60/090538 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/088026 60/089532 60/089599 APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090429 FILING DATE: 19/98-06-11 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-17 1998-06-23 1998-06-17 1998-06-24 1998-06-24 1998-06-24 1998-05-1 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: FILING DATE: 104 PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC17
CURRENT APPLICATION NUMBER: U5/10/121,049
CURRENT APPLICATION NUMBER: U5/202-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Best Local Similarity 25.3%; Pred. No. 6.6e-13;
Matches 87; Conservative 53; Mismatches 138; Indels
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                  Application US/10121049
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Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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                                                                                                                       DeForge, Laura
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US-10-121-049-260
US-10-121-049-260
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46 QADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQ-IQTNVIHSAYEHGVKK- 103
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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53; Mismatches 138; Indels
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13.1%; Score 215;
Best Local Similarity · 25.3%; Pred. No. 6
Matches 87; Conservative 53: Migmatch
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/123,904 CURRENT FILING DATE: 2002-04-16
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                                                                                                                                            Smith, Victoria
Stewart, Timothy A.
                       Gerritsen, Mary E.
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Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
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                                                                        Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
                                              Goddard, Audrey
Gao, Wei-Qiang
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US-10-123-904-260
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CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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; ORGANISM: Homo Sapien
US-10-175-746-260
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; ORGANISM: Homo Sapien
US-10-176-918-260
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                                                                                                                        APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCREED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140, 470
CURRENT APPLICATION NUMBER: US/002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
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53; Mismatches 138; Indels
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                             tewart, Timothy A.
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Stewart, Timothy A
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Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                  Watanabe, Colin K
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APPLICANT: Beresini, Maureen
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Gurney, Austin L.
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Best Local Similarity 25.35
Matches 87; Conservative
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                                                                 rumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapien
US-10-140-470-260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 VGARLÍLLASTSEVÝGD.-PEVHPQSEDÝWGHVNPIGPRACÝDEGKRVAETMCYAÝMKÓEG 250
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NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                          13.1%; Score 215; DB 9; L 25.3%; Pred. No. 6.6e-13; ive 53; Mismatches 138;
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Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550
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CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 260, Application US/10176918; Publication No. US20030027275A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stewart, Timothy A.
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Wood, William
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Filvaroff, Ellen
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Best Local Similarity 25.3
Matches 87; Conservative
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46 QADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQ-IQTNVIHSAYEHGVKK- 103
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TITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC288
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                Length 420;
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                                                    53; Mismatches 138; Indels
                                                                                     1 MSDKSAK-IFVAGHRGLVGSAIVRKLQEQGFTNLVLKT------
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 260
LENGTH: 420
                13.1%; Score 215; DB 9; 25.3%; Pred. No. 6.6e-13;
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CURRENT FILING DATE: 2002-06-20
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o. US20030027276A1
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Watanabe, Colin K
Wood, William
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                               Best Local Similarity 25.34
Matches 87; Conservative
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Filvaroff, Ellen
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US-10-176-921-260
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                  Query Match
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143 HDVVEPLYIEVDQIYHLASPAS------PPNYMYNPIKTLKTNTIGTLNMLGLAKR 192
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                                                                                             104 ---- LLFLGSSCIYPKFAPQPIPESALLTASLEP--TNEWYAIAKIAGIKTCQAYRIQHG
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CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT FILING DATE: 2002-08-26
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PRIOR APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 00/105913
PRIOR PLING DATE: 2002-04-09
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PELING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/06973
PRIOR PELING DATE: 1997-10-21
PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-05-06
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-05-06
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PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-08
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Watanabe, Colin L.
Wood, William I.
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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PRILING DATE: 1998-05-22

R APPLICATION NUMBER: 60/089532

R PILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08905

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/090472

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/09055

R FILING DATE: 1998-06-24

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R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-27

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090691
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R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/106178
R FILING DATE: 1998-10-28
R APPLICATION NUMBER: 60/106248
R FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R APPLICATION NUMBER: 60/098544
R FILING DATE: 1998-08-31
R APPLICATION NUMBER: 60/099596
R FILING DATE: 1998-09-09
R APPLICATION NUMBER: 60/099598
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R APPLICATION NUMBER: 60/100385
R FILING DATE: 1998-09-15
R FILING DATE: 1998-09-15
R FILING DATE: 1998-09-15
R APPLICATION NUMBER: 60/10057
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/095302
FILING DATE: 1998-08-04
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APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100919
FILING DATE: 1998-09-17
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FILING DATE: 1998-08-04
APPLICATION NUMBER: 60/095916
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FILING DATE: 1998-08-11
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R APPLICATION NUMBER: 60/115565
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Best Local Similarity 25.3%; Pred. No. 6.6e-13;
Matches 87; Conservative 53; Mismatches 138; Indels 66; Gaps
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Searched:

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Result No.

Sequence Sequence S

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Sequence 1, Application US/09318271A

Sequence 1, Application US/09318271A

Patent No. US20020012979A1

GENERAL INFORMATION:

APPLICANT: Berry, Ala

APPLICANT: Severson, David K.

APPLICANT: Severson, David K.

APPLICANT: Severson, David K.

TILE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"

FILE REFERENCE: 3161-24

CURRENT APPLICATION NUMBER: US/09/318,271A

CURRENT PILING DATE: 1999-03-17

EARLIER APPLICATION NUMBER: 60/125,073

EARLIER APPLICATION NUMBER: 60/125,073

EARLIER PILING DATE: 1999-03-18

EARLIER PILING DATE: 1999-03-18

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US-09-735-056-1

US-09-918-995-26997

US-10-097-340-154

US-10-071-311-96

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US-09-318-271-3

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0 US-09-962-805-2

0 US-09-922-17-296

0 US-09-922-217-296

0 US-09-813-263-296

0 US-09-813-263-296

0 US-09-815-343-253

0 US-09-815-343-253

0 US-09-918-944-150

US-09-918-842A-190

US-09-918-842A-190

US-09-918-842A-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 845702 seqs, 674182571 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB
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168

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Gaps

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TITLE OF INVENTION: Moss genes from Physicomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION WNBER: 1309/734,569 CURRENT APPLICATION WNBER: US 60/171,101 PRIOR APPLICATION NUMBER: US 60/171,101 NUMBER OF SEQ ID NOS: 181 NordPerfect 6.1 SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1 SEQ ID NO 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               950 grerecegarcacerrecearrecercacinarirerrencerceacacinecacacacacacaca 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
41.8%; Score 391; DB 10;
Best Local Similarity 65.0%; Pred. No. 3.6e-119;
Matches 596; Conservative 0; Mismatches 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (347)..(1276)
; OTHER INFORMATION: c_pp001064043r
US-09-734-569-147
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Physcomitrella patens
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689
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    426 GATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCAATCTC
                                                                                   450 AATCGCCGGCATCCTTGCGGTCCAGGCGGTGCCCGACAACATGGCCTGCCGTGGATCTC
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COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <UNKnown>
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TITLE OF INVENTION: No. US20030023075A1el Sequences of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
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FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
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Publication No. US20030023075A1
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27386
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STATE: WI
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US-10-114-170-121/c
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                                                                                                                                                                  1130 CfGaCardGGGAractrcraAGCCrGarGGaACrccacGaAaGcrcarcGaraGCAGCAAA 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCACTCGTCAAGCCGATGTTGAATCCTTCTTTTCTCAAGAGAAGCCAGTTTATGTAAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 geagagcecectectecegencerragageceaecaacaaceargeaecearacecaa 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                         CTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGCCAAACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 GAAGCTICTICCTIGGAICATCTGCATTIACCCIAAAITIGCICCTCAGCCAAITCC
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Fatent No. US20020176873A1

GENERAL INFORMATION:

APPLICANT: Behr, Marcel.

APPLICANT: Schoolnik, Gary

APPLICANT: Schoolnik, Gary

APPLICANT: Wilson, Michael A.

TITLE OF INVENTION: Molecular Differences Between Species of TITLE OF INVENTION: Molecular Differences Between Species of TITLE OF INVENTION: Molecular Differences Between Species of TITLE OF INVENTION: Molecular Differences Between Species of TITLE OF INVENTION: MOLECULAR E. 2001-06-27

FILE REFERENCE: STANIO2CON

CURRENT APPLICATION NUMBER: 09/318,191

PRIOR APPLICATION NUMBER: 60/097,936

PRIOR APPLICATION NUMBER: 60/097,936

PRIOR FILING DATE: 1998-08-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 275.2; DB Pred. No. 9.7e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 AAATGGTACTGTGAGAA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                 907 GATTGGTATTTGAAGAA 923
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56.2%;
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Best Local Similarity 56.2<sup>3</sup>
Matches 517; Conservative
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; ORGANISM: M. tuberculosis
US-09-894-844-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-894-844-49
                                                                                        787
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6087 ATTTGGGTCGCAGGACACAAAGGTATGGTCGGCAGCGCCATAATTCGATCGCTTGCCTCC 6028
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/0993964

Publication No. US20030054522A1

GENERAL INFORMATION:

APPLICANT: Rosenthal, Andre

APPLICANT: Rosenthal, Andre

APPLICANT: Broughton, William John

TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic

TITLE OF INVENTION: Plasmid

FILE REFERENCE: CARPO068

CURRENT APPLICATION NUMBER: US/09/939,964

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 09/214,808

PRIOR FILING DATE: 1999-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5670 TTGTGTCAAGCGTATCGTAAGCAATACGGCGCAAACTTCATATCAGCCATGCCGACAAAT 5611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAGCTTGATCTCACTCGTCAAGCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTIGGIGGIATICACGCIAACACCTATCCTGCTGATTTCATTGGTGTCTCCAG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICIAIGGICCIAAIGACAATITCCACCCGGAGAATICICAIGTGCTICCIGCICTIAIG 561
                                                                                       ĠATGTAAĊGCTTĊŤTCATCAACŤAĠĠŤŢĠĠATĊAŤAAATŤAĊĊĆŤŤCACAĀĠĠŢĊŤŢ
                                 GACAGCTCAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTTAGAGATGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGTTGAATCCTTCTTTCTCAAGAAGCCAGTTTATGTAATCCTAGCAGCAGCTAAA
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                                                                                                                                                                                                                          5446
                                                                                                                                                              923
                                                                                                                                                                                                                          5474 GAAAATACATACAACTGGTTTCTTGAAAA
                                                                                                                                                              895 AGCCAAACTTATGATTGGTATTTGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.3
Best Local Similarity 56.6
Matches 512; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 536165
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US-09-939-964-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6194 GrcGaGGrartrraccraacagrrcrrarccrgccgartrrarargagaarara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 ACTIGICAGGCTIATAGGAITCAGCACGGAIGGGAIGCAAICTCIGGCAIGCCIAAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.8%; Score 269.8; DB 9;
57.1%; Pred. No. 3.5e-78;
tive 0; Mismatches 372;
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
                                                            TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                          TELECOMMUNICATION INFORMATION TELEPHONE: (608) 251-500
                                                                                                                     INFORMATION FOR SEQ ID NO: 121
SEQUENCE CHARACTERISTICS:
LENGTH: 14187
                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.1
Matches 530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         682 G-----
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APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Reski, Ralf
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
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Patent No. US20020064816A1
GENERAL INFORMATION:
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Cirpus, Petra
Bischoff, Friedrich
Frank, Markus
Freund, Annette
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Ehrhardt, Thomas
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APPLICANT: Renz, Andrea
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                             <u> AGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGTGGTGTGTGGGGTACAGGT</u>
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APPLICANT: Berry, Alan
APPLICANT: Berry, Alan
APPLICANT: Severeno, David K.

APPLICANT: Severeno, David K.

APPLICANT: Severeno, Bavid K.

APPLICANT: Burlingame, Richard P.

TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLAN
FILE REPERENCE: 3161-24

CURRENT APPLICATION NUMBER: US/09/318,271A

CURRENT FILING DATE: 1999-05-27

EARLIER FILING DATE: 1999-03-17

EARLIER FILING DATE: 1999-03-18

EARLIER FILING DATE: 1999-05-18

EARLIER FILING DATE: 1999-05-18

EARLIER FILING DATE: 1999-05-18

EARLIER FILING DATE: 1998-06-08

NUMBER OF SEQ ID NOS: 15
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Pred. No. 2.1e-76;
0; Mismatches 378;
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Best Local Similarity 56.5%;
Matches 526; Conservative
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US-09-318-271-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGATTTCATTGGTGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCA
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Pred. No. 1.1e-37;
0; Mismatches 397;
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  CURRENT APPLICATION NUMBER: US/09/962,805
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FI 20002114
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
                                                                                                                                                                                  TYPE: DNA
CRGANISM: Helicobacter pylori
US-09-962-805-2
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.4%;
Matches 411; Conservative
                                                                                                                                                                LENGTH: 933
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APPLICANT: NIITYMAEKI, Jaana
APPLICANT: NIITYMAEKI, Jaana
APPLICANT: NAEBINAE, Jarko
TITLE OF INVENTION: GEOF RECOMBINANT ENZYMES FOR PREPARING GDP-L-FUCOSE AND
TITLE OF INVENTION: GIYCANS
FILE REFERENCE: 2242/50463
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                     22.8%; Score 213.6; DB 10; Length 65.5%; Pred. No. 2.5e-60; ive 0; Mismatches 164; Indels
TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 181 SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1 LENGTH: 701
                                                                                                                                                                                                                                                                                         | NAME/KEY: CDS
| LOCATION: (2)..(487)
| OTHER INFORMATION: 20_PPprotl_064_d07
| US-09-734-569-15
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Patent No. US20020058313A1
GENERAL INFORMATION:
APPLICANT: RENKONEN, Risto
APPLICANT: HATTILL, PIRKO
APPLICANT: HIRVAS, Laura
APPLICANT: HORTLING, Solveing
APPLICANT: KALLIOINEN, Tuula
APPLICANT: KAURANEN, Sirkka-Liisa
APPLICANT: JAERVINEN, Nina
                                                                                                                                                                                                                                              ORGANISM: Physicomitrella patens
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Matches 312; Conservative
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US-09-962-805-2
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                                                                                                                                                                                                                              TYPE: DNA
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APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL.
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION WUMBER: US/09/294,093B
PRIOR TILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR APPLICATION NUMBER: 60/082,567
WINDER OF THE APPLICATION NUMBER: APIL 21,1998
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                                                                    810 GAGGAAGATGAGGTCTCCATCAAGGAGGCAGCCGAGGCGGTGGTGGAGGCCATGGACTTC 869
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         718 AGTGGTCAAGAAGTGACTATTAGAGAGTTGGCTGAGTTGGTGAAAGAGAGGTTGTTGGTTTT
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700345468H1
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                                                                                                                                                                                         870 carcecarcecrirgaracaaccaacrecares 907
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Pred. No. 2.2e-09;
0; Mismatches 108;
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Sequence 2058, Application US/09294093B

; Patent No. US20010051335A1

; GENERAL INFORMATION:
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APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleir
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LOCATION: 2, 6, 50
CTHER INFORMATION: a, t,
US-09-294-093B-2068
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Best Local Similarity
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ORGANISM: Zea mays
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LENGTH: 282
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                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Berry, Alan
APPLICANT: Burning, Jeffrey A.
APPLICANT: Jeffrey A.
APPLICA
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Pred. No. 7.4e-23;
0; Mismatches 349; Indels
                             Sequence 5, Application US/09318271A Patent No. US20020012979A1
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Best Local Similarity 48.7%;
Matches 340; Conservative
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SEQ ID NO 5
LENGTH: 1340
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; NAME/KEY: CDS
; LOCATION: (75)..(1040)
US-09-318-271-5
-09-318-271-5
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124 GATCTCACTCGTCAAGCCGATGTTGAATCCTTCTTTTCTCAAGAGAAGCCAGTTTATGTA 183
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APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COMPOUNDS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SEQ ID NOS: 1124
SEQ ID NO 296
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%; Score 58.8; DB 10;
46.4%; Pred. No. 6.4e-09;
tive 0; Mismatches 222;
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CORGANISM: Homo sapiens
US-09-922-217-296
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US-09-833-263-296/c
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Best Local
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                                                                                                                                                                                                                                                                                   APPLICANT: Carrer. Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.4711C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 296
LENGTH: 447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.3%; Score 58.8; DB 9; Length 4 Best Local Similarity 46.4%; Pred. No. 6.4e-09; Matches 192; Conservative 0; Mismatches 222; Indels
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US-09-922-217-296/C
; Sequence 296, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.;
; APPLICANT: Benson, Darin R.;
; APPLICANT: Benson, Darin R.;
; APPLICANT: Reagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
                                                                                                                 King, Gordon E.
Wang, Aljun
Clapper, Jonathan D.
Skeiky, Yasir A. W.
Fanger, Gary R.
Vedvick Thomas S.
                                                                Jiang, Yuqiu
Smith, Carole L.
   Stolk, John A. Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-296
                                                                                  APPLICANT:
APPLICANT:
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Sequence 296, Application US/09833263
; Patent No. US20020110547A1
; Fatent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Glapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILER REFERENCE: 210121-471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 6.4e-09;
0; Mismatches 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.3
Best Local Similarity 46.4
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-296
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Jiang, Yuqiu Smith, Carole Lynn King, Gordon E. Wang, Aijun

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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655 TTGGCTGATGCTTGTTTTTCTTGCTGGATACAGCGGGTTGGAGCATGTTAACATT 714
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                                                           384 gargagacargarccacaargagccrcccacaacaggaarrrrgggracrcgrargcc 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 CTGGTTGAAGGTTTGATGAGCTGATGGAAGGAGAACATG---TCGGCCCATTCAACCTC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          775 TTTGAAGGGAAGCTTGGATGGGATTGCACTAAGCCAGATGGCACACCGAGGAACTTATG 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 CCGAATGCAAACATAGAGTTCAGACCAAACACAGAAGACGACCCTCACAAGAGAAAGCCT 367
                     364 CCTGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            595 GAGGAAGTTGTGGGGGTACAGGTAGTCCGTTGAGGGAGTTCTTGCATGTTGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       603 GAGCCATYCACTGTTTACGGTGATGGGAAGCAGGACAAGGAGTTTCCAATTTGTTTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               715 GGAAGTGGTCAAGAAGTGACTATTAGAGAGTTGGCTGAGTTGGTGAAAGAGGTTGTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed Sequences of Arabidopsis
thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Expressed Sequences of TITLE OF INVENTION: thaliana FILE REFERENCE: 2023US (PARA-012PRV) CURRENT APPLICATION NUMBER: US/09/770,445 CURRENT FILING DATE: 2001-01-26 PRIOR FILING DATE: 2000-01-27 NUMBER: OF SEQ 1D NOS: 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                      Sequence 638, Application US/09770445
Patent No. US20020023281A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                                   An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Ledford, Brooke L.
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Hoffman, Neil
Hurban, Patrick
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Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                Gorlach, Jorn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davis,
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                                                                                                           424 AAGA 427
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 GATCTCACGGATACAGCACAGACCCGCGCCCTGTTTGAGAAGGTCCAACCCACACGTC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 ATCCATCTTGCTGCAATGGTGGGGGCCTGTTCCGGAATATCAAATACAATTTGGACTTC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 TGGAGGAAAAAGGTGCACATGAACGACAACGTCCTGCACTCGGCCTTTGAGGTGGGCGCC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 AAGAAGCTTCTTTCCTTGGATCATCCTGCATTTACCCTAAATTTGCTCCTCAGCCAATT 363
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                                                                                                                                356 ATCCATCTTGCTGCAATGGTGGGGGCCTGTTCCGGAATATCAAATACAATTTGGACTTC 297
                                                                                                                                                                                                                                                                                                                                                                                                            176 gargadecargarceacaardgecereceaeaacageaarrregeraceerargee 117
GATCTCACTCGTCAAGCCGATGTTGAATCCTTCTTTTCTCAAGAGAAGCCAGTTTATGTA 183
                                        416 GATCTCACGGATACAGCACAGACCCGCGCCCTGTTTGAGAAGGTCCAACTCACACACGTC 357
                                                                                                                                                                                244 ATTGGIGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGTGTG 303
                                                                                                                                                                                                                           296 TGGAGGAAAAACGTGCACATGAACGACAACGTCCTGCACTCGGCCTTCGAGGTGGGCGCC 237
                                                                                                                                                                                                                                                                        304 AAGAAGCTTCTTCCTTGGATCATCCTGCATTTACCCTAAATTTGCTCCTCAGCCAATT 363
                                                                                                                                                                                                                                                                                                                      236 CGCAAGGTGTTCCTGCCTGTCCACTGTATCTTCCCTGACAAGACGACCTACCCGATA 177
                                                                                                                                                                                                                                                                                                                                                                   364 CCTGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 AAGATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCAATC 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AAGAGGATGATGGACGTGCAGAACAGGGCCTACTTCCAGCAGTACGGCTGCACCTTCACC
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                                                                                     ATCCTAGCAGCAGCTAAAGTTGGTGGTATTCACGCTAACAACACCTATCCTGCTGATTTC
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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 253
LENGTH: 656
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46.7%; Pred. No. 0.00037;
live 0; Mismatches 162;
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Patent No. US20010055596A1
GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(656)
OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 46.7°
Matches 142; Conservative
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US-09-815-343-253
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Search completed: June 3, 2003, 05:01:27 Job time: 194 secs

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049213 arabidopsis
Q91mu0 arabidopsis
Q95293 mycobacteri
O86299 mycobacteri
Q9rcb2 yersinia ps
Q56873 yersinia en
P71791 mycobacteri
Q8xgf8 salmonella
Q8xf743 salmonella
Q987743 salmonella
Q98540 escherichia
Q98714 arabidopsis
Q98510 paramecium
Q94611 paramecium
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1 MSDKSAKIFVAGHRGLVGSA.....SLRDGLSQTYDWYLKNVCNR 312
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Q9LMU0
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Perfect score:
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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paratuberculosis and M. avium subsp. silvaticum with homologous
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59.2%; Pred. No. 5.5e-78;
ive 50; Mismatches 75; Indels
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InterPro; IPR002198; ADH short.
PROSITE; PS00061; ADH SHÖRT; UNKNOWN 1.
SEQUENCE 328 AA; 35227 MW; 31C4449E9C5BIAC6 CRC64;
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                                                                               89.8%; Score 1478; DB 10;
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ive 19; Mismatches 17;
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Microbiogy 144:3413-3423(1997).
Misrobiology 144:3413-3421;
Misropiogy 1185V.
HSSP; P32055; 1BSV.
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                                                                                                                       Matches 276; Conservative
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A Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
A Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
A Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
Hayaahizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J.; Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
A Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
A Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
T. "Full Length cDNA of gene At1g17890 (GI:15220878).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AC034106; AAF36236.1; -.
R HSSP; P32055; 1BSV.
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STRAIN=CV. COLUMBIA,

SARANO H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,

Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,

Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,

Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,

Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,

Federspiel N.A., Theologis A.;

"The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1.";

Submitted (AUG-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                               1 MSDKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVY
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                                                                                   10; Length 312;
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312 AA, 34477 MW, 4F5E77D9FA492COB CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
87115.12 protein (Putative GDP-L-fucose synthetase)
F2H15.12 OR ATIG17890.
Arabidopsis thaliana (Mouse-ear cress).
                                                                               Score 1646; DB 10;
Pred. No. 4.9e-138;
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ilarity 100.0%;
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SEQUENCE
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                                                     EVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTY 302
                                                                                                                                                                                           LAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIP
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181 IPALLRRFHEAKIRNDKEMYVWGTGKPMREFLHVDDMAAASVHVMELSDQIYQTNTQPML
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                                   ESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skurnik M., Peippo A., Ervela E.,
"Characterization of the O-antigen gene clusters of Yersinia
"Characterization of the O-antigen gene cluster of Yersinia
pseudotubesis and the cryptic O-antigen gene cluster of Yersinia
pestis shows that the plague bacillus is most closely related to and
has evolved from Y. pseudotuberculosis serotype 0:1b.";
Mol. Microbiol. 37:316-330(2000).
EMBL, AJ251712; CAB63301.1;
HSSP; P32055; 1BSV.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pfam; PF01118; Semialdhyde dh; 1.
SEQUENCE 321 AA; 36289 WW; 10F97CCOD2ABCCB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 969; DB 2;
; Pred. No. 7.7e-78;
48; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                             321 AA
                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20392461; PubMed=10931327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 LRDGLSQTYDWYLKNVCN 311
                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, (TrEMBLrel. 13, 1 (TrEMBLrel. 19, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 59.1<sup>†</sup>
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDP-L-fucose synthetase.
                                                                                                                                                                                                                                        DWYLKN 308
                                                                                                                                                                                                                                                                          SWYRTN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=109458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=PA3606;
                                                                                                                                                                                                                                                                                                                                                                              Q9RCB2;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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 88
                                                                   148
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                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yersinia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIP 122
                                                                                                     148 ESALLTGPLEPTNDAYAIAKIAGILQVQAVRRQYGLAWISAMPTNLYGPGDNFSPSGSHL 207
                                                                                                                                                    EVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTY 302
                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=M.avium; STRAIN=2151;
Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
"Identification of a gene cluster involved in glycopeptidollipid
biosynthesis and of a gene cluster encoding daunorubicin resistance in
two strains of Mycobacterium avium serovar 2.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A low 6+C content element in Mycobacterium avium subsp. paratuberculosis and M. avium subsp. silvaticum with homologous genes in M. tuberculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVI
                   ESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHV
                                                                                   LPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=M.avium subsp. silvaticum;
Tizard M., Bull T., Millar D., Doran T., Martin H., Ford J.,
Hermon-Taylor J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.0%; Score 971; DB 2; Length 339;
59.2%; Pred. No. 5.5e-78;
ive 50; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA; 37160 MW; 701B483E2CD3E7AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                             339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium avium subsp. silvaticum, and
                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=44282, 1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium avium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P32055; 1BSV.
                                                                                                                                                                                                                         303 DWYLKN 308
                                                                                                                                                                                                                                                         328 SWYRTN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               GSBB protein.
GSBB OR MERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Simi
Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                   183
                 123
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63 LAAAKVGGIHANNIYPADFIGVNLQIQINVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::|:::|||||||||||::|
11 DRAARVYIAGHRGLVGSALLRTFAGAGFTNLLVRSRAELDLTDRAATFDFVLESRPQVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 DKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CDC 1551 / OSHKOSH,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.";
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO E.COLI WCAG AND TO RHIZOBIUM SP. (STRAIN NGR234)
YAAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Ebrown D., Chillingworth T., Connor F., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculist, Rv1512; -.
Hypothetical protein, Complete proteome.
SEQUENCE 322 AA; 34537 MW, BAF0A55C530BAZA6 CRC64;
                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv1512.
RV1512 OR MT1562 OR MTCY277.34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.0%; Score 955; DB 16;
59.7%; Pred. No. 1.4e-76;
ive 44; Mismatches 78;
                                                                                                                                                                                                                                $
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EMBL; AE007023; AAK45829.1; ALT_INIT.
HSSP; P32055; 1BSV.
                                                                                               305 LKMTYQWFLDNQNN 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dest Local Similarity 59.7.
Aatches 181; Conservative
                                                                                                                                                                                                                                PRELIMINARY;
                                                                      298 LSQTYDWYLKNVCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; MT1562; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 LTGVLEPTNEPYAIAKIAGIKLCESYNRQYNRDYRSVMPTNLYGENDNFHPDNSHVIPAL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLL----DRYSG-----LEHVN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase.";
Microbiology 142:277-288(1996).
-!- FUNCTION: CARRIES OUT BOTH THE EPIMERASE AND REDUCTASE REACTIONS
STEPS TO CONVERT GDP-4-DEHYDRO-6-DEOXY-D-MANNOSE INTO GDP-L-FUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||||||:
185 LRRFHEAKMRNDNEIIVWGSGKPWREFLHVDDMAAASIYVWELADDIYAANTQPMLSHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
-!- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
-!- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCHARIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 IGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97157942; PubMed-9004221; Zhang L., Radziejewska-Lebrecht J., Krajewska-Pietrasik D., Zhang L., Skurnik M.; Toivann P., Skurnik M.; Wille gene cluster directing O-antigen biosynthesis in Yersinia enterocolitica serotype 0:8: identification of the genes for mannose and galactose biosynthesis and the gene for the O-antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang L., Toivanen P., Skurnik M.;
"The gene cluster directing O-antigen biosynthesis in Yersinia
enterocolitica serotype 0.8: identification of the genes for mannose
and galactose biosynthesis and the gene for the O-antigen
                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 33 NADP (POTENTIAL).
321 AA; 36066 MW; F7DA049FC7D4EB62 CRC64;
                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Fucose synthetase (WBCJ protein) (ORF14.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.1%; Score 956.5; DB 2;
58.9%; Pred. No. 9.9e-77;
ive 48; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: TO OTHER FUCOSE SYNTHETASES.
EMBL. U46859; AAC60774.1; -.
Lipopolysaccharide biosynthesis; NADP.
                                                                                                                                       321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 278-321 FROM N.A.
STRAIN-8081C / SEROTYPE O:8;
MEDLINE-97086507; PubMed-8932701;
LEVGLTMTYQWFLAHQNN 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Microbiol. 23:63-76(1997)
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Matches 185; Conservative
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                             Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=8081-C;
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                       301
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                                                                                                                                                                                                                                                                                                                                         Yersinia
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65 KVGGIVANNTYPADFIYQNMMIESNIIHAAHQNDVNKLLFLGSSCIYPKLAKQPMAESEL 124
                                                          125 LQGTLEPTNEPYAIAXIAGIKLCESYNRQYGRDYRSVMPTNLYGPHDNFHPDNSHVIPAL 184
                                                                                                                                                                                                                                                                                        67 KVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL 126
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                                                                                                                                                                                                                                                       238 IGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21156231; PubMed=11258796; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Iida T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
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                                                                                                                                                                        LTASLEPTNEWYALAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL
                                                                                                                                          187 MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLD------RYSGLEHVN
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative nucleotide di-P-sugar epimerase or dehydratase (GDP-fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21074935, Pubmed=11206551,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.A.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / RIMD 0509952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetase chain A).
WCAG OR Z3216 OR ECS2857.
                                                                                                                                                                                                                                                                                                                                                                       298 LSQTYDWYLKN 308
                                                                                                                                                                                                                                                                                                                                                                                                                            305 LAGTYQWFLEN 315
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Q8X4R4
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MEDLINE=21534948; PubMed=11677609;
MCCICLILand M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
LPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQ
                          EVITRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTY
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MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James B.D., Holden M.T.G., Sebainia M., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebainia M., Cronnerton C., Davis B., Davis R.M., Dowd L., White N., Farrar J., Cronnin A., Davis B., Davis R.M., Dowd L., White N., Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JM7-2002 (TrEMBLrel. 21, Last annotation update)
Bifunctional GDP fucose synthetase in colanic acid biosyntheis
(RC 1.-) (GDP-fucose synthetase) (RC 5.1.3.-).
WCAG OR STM2108 OR STY2320.
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EMBL; AL627273; CAD02471.1; -.
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Matches 182; Conservative
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Q9F7A3; Q9F7A3

RESULT 10

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=E.coli 0157:H7, STRAIN=0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takani H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL
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Nature 409:529-533(2001).
                                                                                                                                                                                                                                                         Shimizu T., Yamasaki S., Tsukamoto T., Takeda Y.,; "Analysis of the genes responsible for the O-antigen synthesis in enterohaemorrhagic Escherichia coli 0157."; Microb. Pathog. 26:235-247(1999).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=0157:H7 / EDL933 / ATCC 700927; SPECIES=E.Coli 0157:H7; STRAIN=0157:H7 / EDL933 / ATCC 700927; MEDLINE=21074935; PubMed=11206551; Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Agotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                       gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0157:H7 and genomic comparison with a laboratory strain K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 AA; 36268 MW; 8C8A531115E33791 CRC64;
                                  Last sequence update)
Last annotation update)
(Fucose synthetase).
                   Created)
                                                                                                                                                                                                            SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=184;
MEDLINE=99240837; PubMed=10222209;
                  01-MAY-2000 (TrEMBLrel. 13, Creat. OL-MAY-2000 (TrEMBLrel. 13, Last. OL-MAR-2002 (TrEMBLrel. 20, Last. GDP-L-fucose pathway enzyme (Fucow WBHF OR FCI OR 23197 OR ECS2838. Escherichia coli, and Escherichia coli.
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                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.29
Matches 178; Conservative
                                                                                                                                                                           NCBI_TaxID=562, 83334;
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SEQUENCE 321 AA:
                                                                                                                                                             Escherichia
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297
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                                                                        :|:| : |||||| : :||||:||::|| ::|| CTGVDCTIRELAQTIAKVVGYKGRVVFDASKPDGTPRKLLDVTRLHQLGWYHEISLEAG
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                                                      VFLLDRYSGLEHVN
                                                                                                                         IGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stevenson G., Lan R., Reeves P.R.; "The colanic acid gene cluster of salmonella enterica has a complex
                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.4%; Score 928.5; DB 2
Best Local Similarity 57.9%; Pred. No. 3.1e-74;
Matches 180; Conservative 53; Mismatches 69
                                                      MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADAC-
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                                                                                                                                                                                                                                                                                                                   321 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEMS Microbiol. Lett. 191:11-16(2000).
EMBL; AF285084; AAG24814.1; -.
HSSP; P32055; 1BSV.
                                                                                                                                                                                                                                                                                                                                                      Created)
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MEDLINE=20461159; PubMed=11004393;
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                                                                                                                                                                                            LSQTYDWYLKN 308
                                                                                                                                                                                                                 |: || |:|:|
LASTYQWFLEN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella.
NCBI_TaxID=602;
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01-MAR-2001
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Q9S5F8 RESULT 11

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[1] -
SEQUENCE FROM N.A.
STRAIN=NCTC 9343;
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Q8VU14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTASLEPTNEWYALAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                               "Organization of Escherichia coli 0157 O antigen gene cluster and identification of its specific genes."; Infect. Immun. 66:1345-3551(1998).
EMBL, AF061251, AAC32346.1; ---
HSSP; P32055; 1BSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDP-fucose synthetase.
FCL OR ATU4790 OR AGR L 185.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 AA; 36531 MW; 382A03B17CABD6E9 CRC64;
                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.6%; Score 915.5; DB 2;
57.2%; Pred. No. 4.4e-73;
tive 50; Mismatches 74;
                                                                                                                                    323 AA
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MEDLINE=98339851; Pubmed=9673232;
Wang L., Reeves P.R.;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 57.28
Matches 178; Conservative
LSQTYDWYLKN 308
                    LSQTYDWYLKN 308
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LENTYNWFLEN 317
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                                                                                                                                    PRELIMINARY;
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NCBI_TaxID=176299;
[1]
                                                                                                                                                                                                                                 Fucose synthetase Fcl
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
298
                                    305
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                                                                                             RESULT 12
085340
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                                                                                                                                                                                                                                                                                                                                                                                                                      Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
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MEDLINE-21608551; PubMed=11743194;

Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

Goodner B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

Cielo C., Slater S.
SEQUENCE FROM N.A.

MEDLINE=21(60550; PubMed=11743193;

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MEDLINE=21(60550; PubMed=10.C., Raul R., Monks D.E., Kittajima J.P.,

OKUTA V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chapman P., Zhou Y., Chen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.V.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.4%; Score 895.5; DB 16; Length 55.5%; Pred. No. 2.7e-71; ive 59; Mismatches 73; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GDP-4-keto-6-deoxy-D-mamnose-3, 5-epimerase-4-reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 AA; 36726 MW; 4DB36D98CEE75380 CRC64;
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Best Local Similarity 55.5%
Matches 166, Conservative
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Van Etten J.L.;
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                                                                                                                                                                                                LAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIP 122
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Coyne M.J., Comstock L.E., "A Conserved Region of the Bacteroides fragilis Chromosome Upstream of the Polysaccharide B Locus Contains Genes Implicated in the Synthesis
                                                                                                                                                 DKSAKI FVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVI
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MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96187795; PubMed=8614977; MEDLINE=96187795; PubMed=8614977; Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.; "Analyais of 94 kb of the chlorella virus PBCV-1 330-kb genome: map positions 88 to 182."; Virology 216:102-123(1996).
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                                                                                                                                                                                                                                                                                                                                                                                               253 VKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDWYL 306
                                                                                                                                                                                                                                                                                                                                                                                                             Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBI_TaxID=10506;
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MEDLINE=20013326; PubMed=10544099;
Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R.,
Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                Length 360;
                                                                                                                       67; Indels
                                   of GDP-L-fucose.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF285774; AAL61890.1; -.
SEQUENCE 360 AA; 40949 MW; FBB327E10A1843B2 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                Query Match 54.3%; Score 893; DB 2; Best Local Similarity 51.7%; Pred. No. 5.2e-71; Matches 183; Conservative 54; Mismatches 67;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
PBCV-1 fucose synthase.
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64 LAAAKVGGIHANNSFGGDFIRDNLMIQTNVIHASKTFNVKKLVFLGSSCIYPKESPNPIK 123
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SEQUENCE J., Graves M.V., Van Etten J.L.;

Submitted (DEC-20000) to the EMBL/GenBank/DDBJ databases.

Submitted AACS6663.1;

HSSP; P32055; 1BSV.

HSSP; P32055; 1ASV.

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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 882; DB 54.6%; Pred. No. 4.1e ive 57; Mismatches
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Matches 167; Conservative
                                                         Van Etten J.L.;
Submitted (MAY-1997)
                                                                                                                                        Van Etten J.L.;
Submitted (SEP-1997)
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EDFTKN 309
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Job time : 67 secs
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SEQUENCE FROM N.A.
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3, 2003, 05:01:31 ; Search time 35 Seconds (without alignments) 856.970 Million cell updates/sec June Run on:

US-10-089-014-1 1646 Perfect score:

1 MSDKSAKIFVAGHRGLVGSA.....SLRDGLSQTYDWYLKNVCNR 312 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB		Description
1	1646	100.0	312		F96758	hypothetical prote
7	1478	89.8	328	7	B86314	F2H15.12 protein -
m	955	58.0	322	Н	C70714	
4	944.5	57.4	m	~	A10768	GDP-fucose synthet
ហ	<u>.</u>	57.4	m	7	A98986	
9		57.4		~	D85831	GDP-fucose synthet
7	w.	57.3	321	Н	C64971	hypothetical 36.1
80	'n.	55.6	321	~	A85829	fucose synthetase
σ		55.6		7	F90983	fucose synthetase
10	895.5	54.4		N	A98142	hypothetical 34.7K
11	895.5	4		~	AB3146	>
12	882	53.6		7	T17792	hypothetical prote
13	877.5	53.3		N	F97168	nucleoside-diphosp
14	989	41.7		~	D81288	probable fucose sy
15	596.5	36.2		N	AH3615	gdp-4-dehydro-D-rh
16	567.5	34.5		~	AB2409	dTDP-glucose dehyd
17	565.5	34.4	312	Н	S74432	hypothetical prote
18	547.5	33.3		~	T44323	ы
19	505	30.7		~	E64525	nodulation protein
	495	30.1		~	E71981	probable sugar nuc
	401	24.4		-1	812516	hypothetical prote
22		22.2		N	T16645	hypothetical prote
	345.5	21.0		N	AI3615	>
24	270.5	16.4	310	7	E90231	UDP-glucose 4-epim
	266	16.2		7	C72368	_
	264.5	16.1		7	S75771	
27	φ	16.0	m	7	C69149	conserved hypothet
28	25	15.7	m	7	920	probable DTDP-Gluc
29	253.5	15.4	321	7	G70415	nucleotide sugar e

udp-glucose 4-epim	UDFGIUCOSE 4-Epime probable sugar-nuc	probable UDP-gluco	hypothetical prote	. nucleotide sugar e	FUSION, Nucleoside	hypothetical prote	probable UDP-gluco	UDP-glucose 4-epim	UDP-glucose 4-epim	nucleotide sugar e	dTDP-Glucose 4,6-d	probable epimerase	dTDP-glucose 4-6-d	probable UDP-gluco
D75143	D86934	A71183	T44339	S70889	Н96989	C72353	D75486	C84072	A75303	E84113	F90233	G95920	G82785	H71145
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253	250 246	245	243	240	236	231.5	231	230	227.5	226.5	226	224.5	223.5	221.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Pypothetical protein T18K17.8 [imported] - Arabidopsis thaliana CSP5/SE Protess Arabidopsis thaliana (mouse-ear cress) Cjate: 02-Mar-2001 #text_change 31-Dec-2001 Cjate: 02-Mar-2001 Mr.; Conn, L.; Conn, C.; Chan, S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. P.; Southwick, A.M.; Sun, H.; Tallon, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, P.; Southwick, A.M.; Sun, H.; Tallon, R.; Reference number: A86141; MUID:21016719; PMID:11130712 Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712 Arabidopsis.
A;Residues: 1-312 <STO>
A;Cross-references: GB:AE005173; NID:g6598858; PIDN:AAF18712.1; GSPDB:GN00141 C;Genetics:
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C;Superfamily: Escherichia coli probable UDPglucose 4-epimerase
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100.0%; Score 1646; DB 2; Length
Best Local Similarity 100.0%; Pred. No. 6e-131;
Matches 312; Conservative 0; Mismatches 0; Indels
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61 VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKILFLGSSCIYPKFAPQP 120

61 VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: 1-322 <CCL> A;CCOS + CCOS + CCCL> A;CXOS + CCCL> A;CXOS + CCCL> A;EXperimental source: strain H37RV C;Genetics: A;Gene: epih C;Superfamily: Escherichia coli probable UDPglucose 4-epimerase
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A10768
CDP-fucose synthetase (EC 5.1.3.-) [imported] - Salmonella enterica subsp. enterica serviceses synthetase (EC 5.1.3.-) [imported] - Salmonella enterica subsp. enterica servar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: A10768
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, K.P.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero, A;Accession: A1776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ESALLTGPLEPTNDAYAIAKIAGILAVQAVRRQHGLPWISAMPTNLYGPGDNFSPSGSHL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 DHTIGEIAEMVASAVGYSGETRWDPSKPDGTPRKLLDVSVLREAGWRPSIALRDGIEATV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL513382; PIDN:CAD02471.1; PID:g16503337; GSPDB:GN00176
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                               11 DRAARVYIAGHRGLVGSALLRTFAGAGFTNLLVRSRAELDLTDRAATFDFVLESRPQVVI
                                                                                                                                                                                                                                                                                                                                                                                                                  63 LAAAKVGGIHANNIYPADFIGVNLQIQINVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIP
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                                                                                                                                                                                                                Query Match 58.0%; Score 955; DB 1; Length 322; Best Local Similarity 59.7%; Pred. No. 9.6e-73; Matches 181; Conservative 44; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli probable UDPglucose 4-epimerase
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58.5%; Pred. No. 7.4e-72;
ive 53; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 AWY 313
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Keywords: isomerase
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C;Superfamily: E
C;Keywords: isom
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R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Vi. Lin, X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Reference number: A86141; MUID:21016719; PMID:11130712

A.Accession: B86314

A.Accession: B86314

A.Accession: Preliminary

A.Residues: 1-328 <STO>
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C;Species: Mycobacterium tuberculosis
C;Date: 10-8ep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: C70714
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Richardander, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Rieference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70714
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A,Map position: 1
C,Superfamily: Escherichia coli probable UDPglucose 4-epimerase
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                                                                                                                                        F2H15.12 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 14-Dec-2001
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                             312
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TYEWYLENVVQK 326
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                           TYDWYLKNVCNR
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nes 276; Conserv
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C;Accession: D85831
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Reference number: A88480; MUD:21074935; PMID:11206551
A;Reference number: A885480; MUD:21074935; PMID:11206551
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-321 <8TO>
A;Residues: 1-321 <8TO>
A;Residues: 1-321 <8TO>
A;Residues: 1-321 <8TO>
A;Residues: 1-321 <8TO
A;Residues: C;Genetics: Strain O157:H7, substrain EDL933
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N'Alternate names: cpsB 5'-region hypothetical protein 2
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Accession: C64971; D55239
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.
Science 277, 1453-1462, 1997
A;File: The complete genome sequence of Escherichia coli K-12.
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A,Residues: 1-321 cBLAT>
A,Cross-references: GB:AE000295, GB:U00096; NID:g1788354; PIDN:AAC75113.1; PID:g1788365, B,Cxoss-references: GB:AE000295, GB:U00096; NID:g1788354; PIDN:AAC75113.1; PID:g1788365, B,Experimental source: strain K-12, substrain MG1655
B,AOyama, K. J. Haase, A.M.; Reeves, P.R.
Mol. Biol. Evol. 11, 829-838, 1994
A,Title: Evidence for effect of random genetic drift on G+C content after lateral transf A,Title: Evidence for effect of random genetic drift on G+C content after lateral transf A,Reference number: A55239; MUID:95115532; PMID:7815923
A,Status: nucleic acid sequence not shown; translation not shown
A,Residues: 1-254, DV, 257-321 cAOY>
A,Cross-references: GB:U38473; GB:L11721; NID:g3041811; PIDN:AAC77843.1; PID:g1407613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 KVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL 126
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
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C;Superfamily: Escherichia coli probable UDPglucose 4-epimerase
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                                                                                                                                                                                                                                                                                                                                                                                                                             57.4%; Score 944.5; DB 2;
57.9%; Pred. No. 7.4e-72;
tive 55; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.9
Matches 180; Conservative
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305 LASTYQWFLEN 315
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D85831
D85831
GDP-fucose synthetase wcaG [similarity] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Dec-2001
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                                                                                                                                                                                                                                          238 IGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG 297
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Best Local Similarity 57.9%; Pred. No. 7.4e-72;
Matches 180; Conservative 55; Mismatches 67
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LAGTYQWFLEN 315
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LASTYQWFLEN 315
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fucose synthetase [imported] - Escherichia coli (strain O157:H7, substrain RIMD O509952), C;Species: Escherichia coli (c;Species: Bacherichia coli (c;Species: Bacherichia coli (c;Species: Bacherichia coli (c;Species: Bacherichia coli (d;Species: Bacherichia coli (d;Species: Bacherichia coli (d;Species: Bacherichia (d;Species: Bacherichia (d;Species: Bacherichia (d;Species: Bacherichia (d;Species: Bacherichia (d;Species: Bacherichia coli (d;Species
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A;Cross-references: GB:BA000007; PIDN:BAB36261.1; PID:g13362306; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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C;Superfamily: Escherichia coli probable UDPglucose 4-epimerase
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                                                                                                              298 LSQTYDWYLKN 308
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LENTYNWFLEN 315
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Dec-2001
C;Accession: A85829
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 2529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Retaus: preliminary
A;Molecule type: DNA
A;Retaus: preliminary
A;Molecule type: DNA
A;Retainental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Ci
C;Superfamily: Escherichia coli probable UDPglucose 4-epimerase
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LRRFHDAVENNSPNVVVWGSGTPKREFLHVDDMASASIYVMEMPYDIWQKNTKVMLSHIN 244
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                                                                                                                                                                                           99
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LRRFHEATAQNAPDVVVVWGSGTPMREFLHVDDMAAASIHVMELAHEVWLENTQPMLSHIN
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                                 C; Superfamily: Bscherichia coli probable UDPglucose 4-epimerase
                                                                                                                                       Indels
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                                                                                     DB 1;
                                                                                  Score 943.5; DB :
Pred. No. 8.9e-72
                                                                                                                                       56; Mismatches
                                                                               Query Match
Best Local Similarity 57.6%;
Matches 179; Conservative 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSQTYDWYLKN 308
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LASTYQWFLEN 315
                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       127
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A;Gene: yefB
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64 LAAAKVGGIHANNSFGGDFIRDNLMIQTNVIHASKTFNVKKLVFLGSSCIYPKESFNPIK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTY 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 RNLAHLIAGIVGYEGQIVFDTSKPDGAPRKLLDCSRLNALGWNSTVELRYGIQDLYEWW 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                     247 RELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDWY 305
                                                                                                                                                                                                                                  hypothetical protein A295L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T17792
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
                      3 DKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQ
  MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVN1GSGQEVT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: Escherichia coli probable UDPglucose 4-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96663.1
A;Experimental source: specific host Chlorella strain NC64A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.6%; Score 882; DB 2;
54.6%; Pred. No. 1.3e-66;
iive 57; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                A;Reference number: Z18806
A;Accession: T17792
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-317 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.6
Matches 167; Conservative
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C;Sunerf--
187
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Fixed, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Ritle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:11743193
A/ROIscule type: DNA
A/ROIscule type: C/Genetics:
A/Genetics:
A/Gene: fcl
A/Map position: linear chromosome
C;Superfamily: Escherichia coli probable UDPglucose 4-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDP-fucose synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                 . 99
               Cross-references: GB:AE007870; PIDN:AAK88659.1; PID:g15158384; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQEVTI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVGGIHANNIYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 LTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL 186
                                                                                                                                                                                                                                                           18 RVWVAGHTGMVGSALVRRLEREN-CEILKVSRRELDLTRQYETEQWMAAARPQVIFVAAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDWY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA
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                                                                                                                                                                                                                                    7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA
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                                                                                                                                                   Length 331;
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                                      C;Genetics:
A;Gene: AGR_L_185
A;Map position: linear chromosome
C;Superfamily: Escherichia coli probable UDPglucose 4-epimerase
                                                                                                                                                                                           Indels
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                                                                                                                                              54.4%; Score 895.5; DB 2;
llarity 55.5%; Pred. No. 1e-67;
Conservative 59; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.4%; Score 895.5; DB 2; Best Local Similarity 55.5%; Pred. No. 1e-67; Matches 166; Conservative 59; Mismatches 73;
                                                                                                                                              Query Match
Best Local Similarity
Matches 166; Conserv
«KUR»
A; Residues: 1-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3615
C;Accession: AH3615
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes:
Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten:
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                               gdp-4-dehydro-D-rhamnose reductase (EC 1.1.1.187) [imported] - Brucella melitensis (str:
                                                              243 SDDLADVAIYTWQNIDFKDLIKDRKSKNTHINIGTGIDYSIKEVALMVKNIVGFSGELVF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A,Residues: 1-246 <KUR>
A,Cross-references: GB:AE008918; PIDN:AAL54091.1; PID:g17985049; GSPDB:GN00191
A,Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                             --- DRYSGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 KIFVAGHTGMVGSAILRRLQHED-CDIITAAHSVLDLTRQGPTENFISGHRPDVIIIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHABLDLTRQADVESFFSQEKPVYVILAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                              266 DCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDWY 305
                                                                                                                                                                               303 NTSRPDSTMDRLMDCSKIHSLGWKHKIELKDGIKMMYEWY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5;
.1e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 596.5; 53.2%; Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
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Best Local Similarity 53.2%
Matches 124; Conservative
                                216 VDDLADACVFLL---
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A;Gene: BMEII0849
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C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Accession: D81288
A; Reference number: A81250; MUD:20150912; PMID:10688204
A; Reference number: A81250; MUD:20150912; PMID:10688204
A; Residues: 1-346 <PAR>
A; Residues: 1-346 <PAR>
A; Residues: 1-346 <PAR>
A; Residues: 1-346 <PAR>
A; Cross=references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73852.1; PID:g696885
C; Genetics: A; Genetics: Genetics: A; Genetics: G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable fucose synthetase Cj1428c [imported] - Campylobacter jejuni (strain NCTC 11168)
C.Species: Campylobarter islini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AALIRRFHEAKVSGSQEISIMGSGEQYREFTYIEDLADGIIFLMEHGEKVKGFLNIGCGK 242
                                                                                                                                                                                                                                                                                                                                                                                                              SAAKVGGIQANISNPVDFLMDNLIIEYNVIKNSFEVGIENLLFLGSSCIYPKEAPQPLKE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                             AAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 PALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLE-HVNIGSGQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTY 302
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                                                                                                                                              Length 309;
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                          C;Genetics:
A;Gene: CAC2179
C;Superfamily: Bscherichia coli probable UDPglucose 4-epimerase
                                                                                                                                                                                                       Indels
Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                           Query Match 53.3%; Score 877.5; DB 2; Best Local Similarity 53.6%; Pred. No. 3.1e-66; Matches 164; Conservative 66; Mismatches 75;
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Appl Appli
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Sequence 108, App
Sequence 16, Appl
  Sequence 2
Sequence 6
Sequence 1
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US-08-722-184-2
US-09-043-937A-6
US-08-722-184-10
US-09-043-937A-14
US-09-043-937A-14
US-09-194-612A-11
US-09-1043-937A-10
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US-09-041-986-25
PCT-US94-05277-2
US-09-041-886-25
PCT-US94-05-116
US-09-475-316A-108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,972
FILING DATE: Herewith
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING APPLICATION NUMBER:
RILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: BILLOW J.
TELEPHONE: 650-855-555
                                                                                                                                                                                                                                                                                                                   ratent No. 5932443
; GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION:
APPLICANT: Shah, Purvi
TITLE OF INVENTION:
APPLICANT: Shah, Purvi
TITLE OF INVENTION:
ANTIGENS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 23174 Porter Drive
CITY: Palo Alto
COUNTRY: USA
ZIP. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.2%; Score 463.5;
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                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/08937972 ; Patent No. 5932443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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    335
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181
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LIBRARY: BLADNOT04
CLONE: 1318190
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US-08-937-972-3
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  Query Match
    Appli
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                                                                                          June 3, 2003, 05:02:36 ; Search time 21 Seconds (without alignments) 437.141 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26,
Sequence 26,
Sequence 15,
Sequence 14,
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Sequence 12,
                                                                                                                                                                        1 MSDKSAKIFVAGHRGLVGSA......SLRDGLSQTYDWYLKNVCNR 312
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Sequence 4,
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Sequence 9,
Sequence 8,
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Sequence 7
Sequence 2
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/cgn2_6/prodata/1/iaa/PcTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-370-700-26
US-09-320-87-14
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US-09-614-183-2
PCT-US95-05785-2
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US-09-392-772-6
US-09-392-772-4
US-09-392-772-4
US-09-376-626A-33
US-08-576-626A-32
US-08-576-626A-32
US-09-638-715-4
US-08-576-626A-32
US-09-638-715-4
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                                                                                                                                                                                                                                      262574 segs, 29422922 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                      Issued Patents AA:*
                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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1646
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Match Length
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203.5
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Maximum DB
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2311 RFVHGDIRDAGLLARELKGVDAIVHFAAESHVDRSIAGASV------FTETNVQ 2358
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                                                                                                                                                                                                                                                    66 VIHLAAMVGGLFRNIKYNLDFWRKNVHINDNVLHSAFEVGARKVVSCLSTCIFPDKTTYP 125
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                                                                                                                                                                            5 SAKIFVAGHRGLVGSAIVRKLQEQGF----TNLVLKTHAELDLTRQADVESFFSQEKPVY
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Sequence 4, Application US/09105537A

Batel No. 6265202

GENERAL INFORMATION:

APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Liu, H.

APPLICANT: Liu, H.

APPLICANT: Alao, L.

TITLE OF INVENTION: DNA encoding methymycin and pikromycin

FILE REFERENCE: 600-439831

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT APPLICATION NUMBER: US/09/105,537A

SOFTWARE: FattseQ for Windows Version 3.0

SOFTWARE: FattseQ for Windows Version 3.0
                                                                              Length 271;
                                                                            24.4%; Score 402; DB 2; Length 27 37.3%; Pred. No. 1.8e-35; Live 47; Mismatches 110; Indels
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                                                                          Query Match
Best Local Similarity 37.3'
Matches 98; Conservative
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Matches 84; Conservative
     GenBank
                       199586
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   LIBRARY:
                     ; CLONE: 1
US-08-937-972-6
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                                                                                                                                                                                                                                 HVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHV--NI 238
                                                                                                                                                                                                                                                                                                                                                              GSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLAS----LGWTPKVSL 294
                                                                                                                                                                                                                                                                                                                                                                                    245 GEEDEVSIKEAAEAVVEAMDFHGEVTFDTTKSDGQFKKTASNSKLRTYLPDFRFTP---F 301
                                                                                               65
                                                                                            SMRILVTGGSGLVGKAI-QKVVADGAGLPGEDWVFVSSKDADLTDTAQTRALFEKVQPTH
                                                                                                                                 61 VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
                                                                                                                                                      5 SAKIFVAGHRGLVGSAIVRKLQEQGF----TNLVLKTHAELDLTRQADVESFFSQEKPVY
                       Gaps
                     15;
 35.4%; Pred. No. 4.8e-42; ative 64; Mismatches 124; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto COUNTRY: USA
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Patent No. 5932443
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
ITLE OF INVENTION: ANTIGENS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : : | |: |
KQAVKETCAWFTDN 315
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LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                     111; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
Matches 111; Conserv
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                          227 IQLVADSGRAGEIYNIGGGTELTNNELTERLLAELG----LDWSVVRP-VTDRKGHDRRY 281
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                                                                                                                                                                                                                                                                                                            APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
IIIE REFERENCE: 50489 DIVI
CURRENT APPLICANT: Waldron, Clive
IIIE REPERENCE: 50489 DIVI
EARLIER APPLICATION NUMBER: US/09/370,700
CURRENT APPLICATION NUMBER: US 09/36987
EARLIER PILING DATE: 1998-08-09
EARLIER PILING DATE: 1998-08-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
223 CVFLLDRYSGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRK--
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                                                                                                                 282 SVDHSKIVEELGYAPQVDFETGLRETIRWYQDN 314
                                                                                       LMDSSKLA-SLGWTPKVSLRDGLSQTYDWYLKN 308
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PAPPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MODANIEL, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Saccharopolyspora spinosa
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Best Local Similarity
Matches 89; Conserv
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                                                                                                                                                                                                                                                                   APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                           Length 329;
                   ---RKLMDSSKL-ASLGWTPKVSLRDGLSQTYDWYLKN
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.4%; Score 203.5; DB 4; Best Local Similarity 26.7%; Pred. No. 1e-13; Matches 89; Conservative 45; Mismatches 148;
                                                                                                                                                                         Sequence 26, Application US/09036987A Patent No. 6143526 GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 28,479
REPERENCE/DOCKET UNMBER: 50,
TELECOMMUNICATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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amino acid
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REGISTRATION NUMBER: 28
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INFORMATION FOR SEQ ID NO
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CITY: Indianapolis
STATE: Indiana
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                   268 TKPDGTP--
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US-09-036-987A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 LLQCAVDAGVGRVVHVSTDEVYGSIDSGSWTES----SPLEP-NSPYAASKAGSDLVARA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 YRIOHGWDAISGMPTNLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLR 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 YHRTYGLDVRITRCCNNYGPYQ--HPEK-----LIPLFVTNLLDGG-TLPLYGDGANVR 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------RQADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTN 91
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                        INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
APPLICANT: She, D.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT APPLICATION DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
12.4%; Score 203.5; DB 3;
Best Local Similarity 24.5%; Pred. No. 1e-13;
Matches 84; Conservative 49; Mismatches 139;
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                                   TILE OF INVENTIOUS INCUCRIBERY INTEGRALIAL FOREST

CURRENT APPLICATION NUMBER: US/09/320,878A

CURRENT APPLICATION NUMBER: US/09/320,878A

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER FILING DATE: 1999-05-08

EARLIER FILING DATE: 1999-02-08

EARLIER FILING DATE: 1998-02-08

EARLIER APPLICATION NUMBER: 60/100,880

EARLIER FILING DATE: 1998-05-22

EARLIER FILING DATE: 1998-05-28

WUMBER OF SEC ID NOS: 34
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Patent No. 6265202
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LENGTH: 337
TYPE: PRT
ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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ISOLATION OF THE BIOSYNTHESIS GENES FOR PSEUDO-OLIGOSACHARIDES FROM STREPTOMYCES GLAUCESCENS GLA.O AND THEIR USE
                                                                                                                                                                                                       62 GDIRDAGLLARELRGVDAIVHFAAESHVDRSIAGASV------FTETNVQGTQT 109
                                                                                                                                                                                                                                                92 VIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQA 151
                                                                                                                                                                                                                                                                                      110 LLQCAVDAGVGRVVHVSTDEVYGSIDSGSWTES----SPLEP-NSPYAASKAGSDLVARA 164
                                                                                                                                                                                                                                                                                                                                152 YRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLR 211
                                                                                                                                                                                                                                                                                                                                                        EFLHVDDLADACVFLLDRYSGLEHVNIGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPD 271
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                                                                                                          ------RQADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTN
                                          Gaps
                                        71;
    Length 337;
                                          Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,905
FILING DATE: 29-JUL-1998
CLASSIFICATION: 435
  Score 199.5; DB 4;
Pred. No. 2.8e-13;
0; Mismatches 139;
                                                                                  7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELD-LT
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APPLICATION NUMBER: WO PCT/EP97/02826
FILING DATE: 30-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19622783.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09194905
                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELECOMMUNICATION INFORMATION:
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12.1%;
24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ITILE OF INVENTION: PTITLE OF INVENTION: GNUMBER OF SEQUENCES:
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6306627
GENERAL INFORMATION:
APPLICANT: DECKER
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US-09-194-905-11
                                          83;
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R APPLICATION NUMBER: 60/047, 587
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047, 492
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047, 598
R FILING DATE: 1997-05-23
                        LING DATE: 1997-05-23
PLICATION NUMBER: 60/047,618
LING DATE: 1997-05-23
                                                                                                                                                                                                                        FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,672
                                                                                                                            APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
                                                                                                                                                FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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FILING DATE: 1997-05-23
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ING DATE: 1997-04-11
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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                                                                                   APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                        LICATION NUMBER: 60/047,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/047,601
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LICATION NUMBER: 60/043,314
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APPLICATION NUMBER: 60/043,311
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APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60/043,674
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                                                                                                                                                                                                               APPLICATION NUMBER: 60/047,584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 VE--LVRVSGRPGEIYNIGGGTSLPNLELTHRLLALCGAGPERIVHVENRKGHD---- 278
                                                                                                                                                                                                                                                                                                44 TRQADVESFFSQEKPVYVILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKK 103
                                                                                                                                                                                                                                                                                                                                   65 CDTALVDTLAARHDDIVHFAAESHV---DRSITDSGAFTRTNVLGTQVLLDAALRHGVRT 121
                                                                                                                                                                                                                                                                                                                                                                               104 LLFLGSSCIYPKFAPQPIPESALLTAS-LEPTNEWYAIAKIAGIKTCQAYRIQHGWDAIS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 CVFLLDRYSGL--EHVNIGSGQEVTIRELAELV-----KEVVGFEGKLGWDCTKPDG 272
                                                                                                                                                                                                                                                    5 ILVTGGAĞFIRSAYVRRLLSPGAPGGVAVTVLDKLTYAGSLARLHAVRDHPGLTFVQGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GMPTNLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADA
                                                                                                                                                                        63
                                                                                                                              Length 325;
                                                                                                                                                                   Indels
                                                                                                                                                                                                               ---FTNLVLKTHA-
                                                                                                                          Query Match 11.6%; Score 190.5; DB 4; Best Local Similarity 25.4%; Pred. No. 2.6e-12; Matches 85; Conservative 50; Mismatches 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 TPRKLMDSSKL-ASLGWTPKVSLRDGLSQTYDWY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
IITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1988-09-08
BARLIER APPLICATION NUMBER: PCT/US98/04493
BARLIER APPLICATION NUMBER: 60/040,162
BARLIER APPLICATION NUMBER: 60/040,163
BARLIER FILING DATE: 1997-03-07
BARLIER APPLICATION NUMBER: 60/040,333
BARLIER APPLICATION NUMBER: 60/040,333
BARLIER APPLICATION NUMBER: 60/038,621
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
                                                                                                                                                                                                             8 IFVAGHRGLVGSAIVRKLQEQG---
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Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LING DATE: 1997-05-23
                                         TOPOLOGY: linear MOLECULE TYPE: protein
TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                US-09-194-905-11
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R APPLICATION NUMBER: 60/056,879
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
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R FILING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,593
R APPLICATION NUMBER: 60/047,614
R APPLICATION NUMBER: 60/043,578
R APPLICATION NUMBER: 60/043,578
R APPLICATION NUMBER: 60/043,578
R APPLICATION NUMBER: 60/043,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/056,631
PILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,845
PILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
APPLICATION NUMBER: 60/056,7761
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,664
FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,876
R FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,595
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,599
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585
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APPLICATION NUMBER: 60/047,586
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,594
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APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
                                                                         APPLICATION NUMBER: 60/056,903
FILING DATE: 1997-08-22
                                                                                                            APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
                                                       FILING DATE: 1997-08-22
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98 IQTNVIHSAYEHGVKK-----LLFLGSSCIYPKFAPQPIPESALLTASLEP--TNEWYAI 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GKRVAETMCYAYMKOEGVEVRVARIFNTFGPRMHMNDG-RVVSNFILQALQ----- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGFEGKLGW------DCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDWYLKN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 LKTNTIGTLNMLGLAKRVGARLLLASTSEVYGD--PEVHPOSEDYWGHVNPIGPRACYDE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 GAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGSGQEVTIRELAELVKEV
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                                                                                                                                                                                                                                                                                                                                                 Length 278;
                                                                                                                                                                                                                                                                                                                                          10.9%; Score 180; DB 4; Length 278 27.8%; Pred. No. 2.8e-11; tive 37; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: JI, H., ET AL.
TITLE OF INVENTION: HUMAN UDP GALACTOSE-4-EPIMERASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CRCCHI, STEWART & OLSTEIN
CITT. ROSELAND
CITT. ROSELAND
STREET: 6 BECKER FARM ROAD
CITT. ROSELAND
STREET: USA
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05
EARLIER PILING DATE: 1997-09-05
EARLIER PELING DATE: 1997-09-05
EARLIER PELING DATE: 1997-09-05
EARLIER PELING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/057,669
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EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
MEDIUM TYPE: 1EM PS/2
MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/462,966
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Patent No. 6153739
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WORD PERFECT 5.1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465
FILING DATE: June 5, 1995
APPLICATION NUMBER: PCT/US
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.8%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORD PERFEC
CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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APPLICANT: JI, H, ET AL.
TITLE OF INVENTION: HUMAN UDP GALACTOSE-4-EPIMERASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.3%; Score 169.5; DB 4; Best Local Similarity 21.9%; Pred. No. 5.5e-10; Matches 80; Conservative 58; Mismatches 135;
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/113,536
FILING DATE: JUL-10-98
APPLICATION NUMBER: 08/462,966
FILING DATE: JUN-05-95
APPLICATION NUMBER: PCT/US95/05785
APPLICATION NUMBER: PCT/US95/05785
ATTORNEY/AGENT INFORMATION:
NAME: JONATHAN L. KLEIN
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: 1119
REFERENCE/DOCKET NUMBER: 1110
REFERENCE/DOCKET NUMBER: PF162C1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKT---
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9505785 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                            TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                   ELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
         CLASSIFICATION:
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STATE: NEW JERSEY
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ZIP: 07068
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PCT-US95-05785-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 VNGAEEVVVWGT-----GSPLREFLHVDDLAD---ACVFLLDRYSGLEHVNIGSGQEVT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 YEHGVKKLLFLGSSCIYPKFAPQPIPESALLTASLEP.-TNEWYAIAKIAGIKTCQAYRI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 QHGWDAI-------SGMPTNLYGPNDNFHPENSHVLPALMRRFHEAK 194
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Patent No. 6451577

GENERAL INFORMATION:

APPLICANT: JI et al.

TITLE OF INVENTION: HUMAN URIDINE DIPHOSPHATE GALACTOSE-4-EPIMERASE
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVE

CITY: ROCKVILLE

STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                    Length 348;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.3%; Score 169.5; DB 4; Best Local Similarity 21.9%; Pred. No. 5.5e-10; Matches 80; Conservative 58; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKT---
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APPLICATION NUMBER: US/09/624,183
FILING DATE: 24-Jul-2000
FILING DATE: 11 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFRENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                 TELEFAX: 201.994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 ----EALNVFGNDYDTEDGTGVRDYIHVVDLAKGHIAALRKLKEQCGCRIYNLGTGTGYS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 YEHGVKKLLFLGSSCIYPKFAPQPIPESALLTASLEP--TNEWYAIAKIAGIKTCQAYRI 154
                                                                                                                                                                                                                                                                                                                                                                                                            120 KAHGVKNLVFSSSATVYGNPQYLPLDEAHPTGGCTNPYGKSKFFIEEMIRDL--CQADKT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 QHGWDAI-------SGMPTNLYGPNDNFHPENSHVLPALMRRFHEAK 194
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                                                                                                                                                        40 ELDLTRQADVESFFSQEKPVYVILAAAKVGGIHA---NNTYPADFIGVNLQIQTNVIHSA 96
                                                         Gaps
                                                      93;
Length 348;
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Sequence 2, Application US/09392772 Patent No. 6346403 GENERAL INFORMATION:
                 SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH: 306
                                                                                                                                                                      69; Conservative
                                                                  TYPE: PRT
ORGANISM: Glycine max
 NUMBER OF SEQ ID NOS:
                                                                                                                                                 Best Local Similarity
Matches 69; Conserv
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US-09-392-772-2
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TYPE: PRT
                                                                                                   US-09-392-772-6
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---WNAVLLRYFNPTGAHASGCIGEDPQGIPNNLM-----PYVSQV--AIGRR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
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Sequence 6, Application US/09392772

Patent No. 6346403

GENERAL INFORMATION:
APPLICANT: Famodu, Layo O.
APPLICANT: Antoni Rafalski
TITLE OF INVENTION: Methionine Metabolic Enzymes
FILE REFERENCE: BB-1241

CURRENT APPLICATION NUMBER: US/09/392,772

CURRENT FILING DATE: 1999-09-07

EARLIER FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.3%; Score 169.5; DB 5; Best Local Similarity 21.9%; Pred. No. 5.5e-10; Matches 80; Conservative 58; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKT---
                                                                                                            CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARC, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-305
TELECOMUNICATION INFORMATION:
TELEPAX: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ 1D NO: 2:
                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05785
FILING DATE: Concurrently
MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: 18M PS/2 OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                      LENGTH: 348 AMINO ACIDS TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
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75 NTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPK----PAPQPIP----- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 G--HIPNVGNPNNEVTVRQLAEIMIKVY---SKVSGEQTPETPTVDVSSKEFYGEGYDDS 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 KQLIERLVFAEGAENGLDFTIVRPFNWIGPRMDFIPGVDGPSEGVPRVLACFSNNLLRRE 202
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                                                                                                                                                                                                                                                   123 ----ESALLTASLEPTNEWYAIAKIAGIKTCOAYRIQHGWDAISGMPTNLYGPNDNFHP
                                                                                                                                                                                  23 NTRPLDTIYSNFIDALPVVKYCSENN-KRLIHFSTCEVYGKTIGAFLPKDSPLRKDPAYY
                                                                                                                                                                                                                                                                                                                                                                              ---ENSHVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLD---RYS
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Length 306;
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                                                             Indels
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APPLICANT: Pamodu, Layo O.
TITLE OF INVENTION: Methionine Metabolic Enzymes
TITLE OF INVENTION: Methionine Metabolic Enzymes
FILE REFERENCE: BB-1241
CURRENT APPLICATION NUMBER: US/09/392,772
CURRENT FILING DATE: 1999-09-07
EARLIER FILING DATE: 1998-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
   DB 4;
                                                                44; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 25.2%; Pred. No. 4.9e-08; Matches 78; Conservative 49; Mismatches 126;
                                4.1e-08;
   9.2%; Score 151.5; 25.7%; Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 PRKLMDSSKL-ASLGWTPKVSLRDGLSQT 301
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96; Gaps 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 KEV-VGFEGKLGWDCTKP------DGTPRKLMDSSKL-ASLGWTPKVSLRDG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 YEHGVKKLLFLGSSCIYPK----FAP--OPI---PESALLTASLEP-----TNEW-YA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 IAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHP---ENSHVLPALMRRFHEAKVN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---FEGKLGWDCTKPDGTPRKLMDSSKL-ASLGWTPKV 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.4%; Score 139; DB 4; Length 427; Best Local Similarity 23.2%; Pred. No. 1.6e-06; Matches 87; Conservative 54; Mismatches 138; Indels
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Famodu, Layo O.
APPLICANT: Famodu, Layo O.
APPLICANT: Famodu, Layo O.
TITLE OF INVENTION: Methionine Metabolic Enzymes
FILE REFERENCE: BB-1241
CURRENT APPLICATION NUMBER: US/09/392,772
CURRENT APPLICATION NUMBER: 60/099,519
EARLIER APPLICATION NUMBER: 60/099,519
EARLIER FILING DATE: 1998-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
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Job time: 27 secs
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Patent No. 6346403
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396 PLKDLLETTLTYQHK 410
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                                                                            298 LSQTYDWYLK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-392-772-4
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A GDP-4-keto-6-deo E. coli 0157 antig Novel human diagno GDP-4-keto-6-deoxy E. coli 0111 antig Novel human diagno Novel human diagno Novel human diagno Antibody productio Amino acid sequenc A GDP-4-keto-6-deo Human GDP-fucose s

ABG25460 ABG18364 ABG34139 AAY28286 AAY54116 AAY81361 ABB59947

AAY54115 AAW88319 ABG18368 AAM00029

AAW88305 ABG28981

321 1162 1162 1162 1264 1321 3321 3321 260

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                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1646
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
S S	Score	Match	Match Length DB	8	QI	Description
-	1646	100.0		22	AAG62614	A thaliana GDP-4-k
7	1515	92.0		21	AAY54114	A GDP-4-keto-6-deo
m	1353	82.2		21	AAG09919	Arabidopsis thalia
4	1353	82.2		21	AAG09918	Arabidopsis thalia
S	1353	82.2		21	AAG09917	Arabidopsis thalia
9	1241	75.4	310	22	AAM00095	GDP-4-keto-6-deoxy
7	971	59.0		18	AAW21770	Protein encoded by
æ	971			18	AAW21771	Protein encoded by
6	943.5			21	AAY81360	Escherichia coli G
10	937.5			20	AAY29659	Escherichia coli Y

21 AAY81361 Human GDP-fucose s 22 ABB59947 Drosophila melanog	ABG18365 Novel numan ABG00133	ABG28975	ABG13190 AAW20804	AAU28305	AAB07566 AAG35197	AAG35196	AAG06774	AAG14539	AAG06773	AAY83788	AAB96739	AAG90108		AAG35198	AAW33273		ALIGNMENTS	; 312 AB.			GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase.	1					.6	5.	& TECHNOLOGY.		
321 2		157																; protein;		st entry)	keto-6-de	-deoxy-D-manne		ana.			2000WO-JP02049	9JP-032904	IND SCI	mi Y;	40.
26.6	25.8	23.1	22.0 20.5	19.7	19.0	16.5	16.0	16.0	10.0	15.9	15.4	15.1	15.1	15.0	14.6	14.6		standard;		1 (first	GDP-4-1	4	, :	s thaliana	7-A1.		٠.,	6	AGENCY OF	, Jigami	1292/
22 451.5 23 437.5	ማ		362	. 6	313	1 (1	263	263	263	262	~	α.	N (1 (2)	7	239.5 239.5		RESULT 1 AAG62614 ID AAG62614 st	AAG62614;	06-SEP-2001	A thaliana	GDD-4-keto.	ar chai	Arabidopsis	WO200138507	31-MAY-2001	30-MAR-2000	9-NOV-1999	(AGEN) AGE	Nakayama K,	WPI; 2001-38 N-PSDB; AAH4

Burlingame RP;

DΚ,

Severson

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Production of ascorbic acid or esters, using microorganisms or plants which have genetic modification in enzymes involved in the ascorbic acid synthesis pathway
                                                                                                          Claim 27; Page 167-168; 187pp; English.
 Running JA,
                        WPI; 2000-105890/09.
N-PSDB; AAZ45315.
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                                The present invention provides the protein and coding sequences of the Arabidopsis thaliana GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase. The sequence can be used for the efficient production of GDP-L-fucose, which is essential to the production of functionally important sugar chains containing L-fucose. The present sequence is the protein of the invention.
                                                                                                                                                                                                                                                                                                                  IPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS
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                                                                                                                                                                                            1 MSDKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVY
                                                                                                                                                                                                              1 MSDKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVY
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                                                                                                                                            Query Match 100.0%; Score 1646; DB 22; Length 312; Best Local Similarity 100.0%; Pred. No. 1.5e-159; Matches 312; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A GDP-4-keto-6-deoxy-D-mannose epimerase/reductase protein.
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L-galactono-gamma-lactone dehydrogenase, ester.
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           Claim 1; Page 24-26; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY54114 standard; Protein; 314 AA.
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99US-0125073.
99US-0125054.
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                                                                                                                       312 AA;
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present sequence represents a GDP-4-keto-6-deoxy-D-mannose epimerase/
                                                                                                                                                                                                                         phosphomannomutases, GDP-D-mannose pyrophosphorylases, GDP-D-mannose:GDP-L-galactose epimerases, GDP-L-galactose phosphorylases, L-galactose dehydrogenases, and L-galactose-1-P-phosphatases, L-galactose dehydrogenases, and L-galactono-gamma-lactone dehydrogenases. The methods can be used for the production of ascorbic acid or esters using microorganisms or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENS 180
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                       reductase. The enzyme catalyses the conversion of GDP-D-mannose to GDP-Laglactose. The enzyme can be modified, and used to produce transgenic microcoganisms, which can be used in fermentation techniques to produce vitamin C (ascorbic acid, L-ascorbic acid). The enzyme is modified to increase its action. Other ascorbic acid pathway enzymes which may be used in the method of the invention include hexokinases, glucose phosphate isomerases, phosphomannose isomerases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VILAAAKVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 314;
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Pred. No. 3.7e-146;
1; Mismatches 5;
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92.5%;
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20-SEP-1999;
990S-0121825.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 8035.
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             99US-0155486.
99US-015559
99US-015559
99US-0156596
99US-0157117.
99US-0157865.
99US-0158029
                                                                                                                                 990S-0158369
990S-0159293
990S-0159293
990S-01592329
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990S-0160761
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             23-SEP-1999;
24-SEP-1999;
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13-0CT-1999;
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14-0CT-1999;
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12-0CT-1999;
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25-OCT-1999;
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9905 - 0146386
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15 MLEKSAKIFVAGHRGLVGSAIVRKLQDQGFTNLVLRTHSELDLTSQSDVESFFATEKPVY

1 MSDKSAKIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVY

82.2%; Score 1353; DB 21; Length 307; 89.5%; Pred. No. 1.3e-129; ive 16; Mismatches 14; Indels 0

Query Match
Best Local Similarity 89.5
Matches 255; Conservative

; 0

HVL.PALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGS

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990S-0151303.
990S-0151303.
990S-0151930.
990S-0152363.
990S-0152363.
990S-0153758.
990S-0154018.
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99US-0139899.
99US-0140353.
99US-0140354.
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99US-0141842.
99US-0142154.
99US-0142055.
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99US-0143542
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990S-0145192.
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99US-0139763.
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99US-0140823.
99US-0140991.
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99US-0142803.
99US-0142920.
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9903-0144814.
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990S-0148684.
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990S-0149175.
990S-0149426.
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99US-0139462
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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04-AUG-1999
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09-AUG-1999
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  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 8034.
                   AAG09917 standard; Protein; 359 AA
                                                                                                                                                                              990S-0126785.
99US-0127462.
99US-0128134.
99US-0128714.
99US-0130875.
99US-0130077.
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99US-0136392.
99US-0137528.
99US-0137528.
99US-0138034.
99US-0138044.
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99US-0139456.
99US-0139457.
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                                            17-OCT-2000 (first entry)
                                                                                             Arabidopsis thaliana
                                                                                                           EP1033405-A2.
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18-JUN-1999;
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                               AAG09917;
      RESULT 5
AAG09917
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This invention relates to nucleic acid molecules AAH88708 - AAH88796

isolated from Physcomitrella patens (a moss), which encode carbohydrate

metabolism related proteins (CMRP) represented in AAM0022 - AAM00110.

Concluded in the invention is a vector containing the CMRP CDNA, and a

concluded in the invention is a vector containing the CMRP CDNA, and a

corprehence of the containing the CMRP CDNA, and a

corprehence of the containing of a plant cell) is

corprehenced in the nucleic acid molecules are suitable for modifying a

carbohydrate production system in a host, e.g., microorganisms and

carbohydrate production system in a host, e.g., microorganisms and

carbohydrate production system in a host, e.g., microorganisms and

carbohydrate production system in a host, e.g., microorganisms and

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carbohydrate production system in a post, e.g., microorganisms and

carbohydrate production system in a post, e.g., microorganisms

carbohydrate production system in post, the generic engineering of Corynebacter xylinum and Chlorella to

capacide in the sequencing of the CWRP cDNA sequences of the invention.
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                    247 HVLPALMRRFHEAKANNADEVVVWGSGSPLREFLHVDDLADACVFLMDQYSGFEHVNVGS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals such as carbohydrates, cofactors and enzymes from microorganisms and plants
HVLPALMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEHVNIGS
                                                                                                                                                                                                                                                                                                                                       carbohydrate metabolism related protein; CMRP; sugar; cofactor;
                                                                                                                                                                                                                                                                                                    GDP-4-keto-6-deoxy-D-mannose 3,5-epimerase-4-reductase sequence #163
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                                                                   GOEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLAS 285
                                                                                                      351
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Reski R;
                                                                                      fine chemical production; carbohydrate; polysaccharide.
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Schmidt R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 30; Page 127; 133pp; English.
                                                                                                                                                                                             AAM00095 standard; Protein; 310 AA
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Frank M, Freund A, Duwenig E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-2000; 2000WO-EP12697.
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                                                                                                                                                                                                                                                                                                                                                                                        Physcomitrella patens.
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Best Local Similarity
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; Pred. No. 1.6e-129;
16; Mismatches 14;
                                                                                                                                                                                       990S-0152363.
990S-0153070.
990S-0154018.
990S-0154018.
990S-0154779.
                                                                99US-0150884.
99US-0151065.
99US-0151066.
99US-0151080.
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99US-0158369.
99US-0159293.
              99US-0149902.
99US-0149930.
99US-0150566.
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99US-0155659.
99US-0156458.
99US-0156596.
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Best Local Similarity 89.5%;
Matches 255; Conservative 1
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99US-0160741
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Tizard M;
                                                                                                                                                                                   Similarity
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                                                                                                                                                                                     DKSAKI FVAGHRGLVGSA I VRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVI
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mycobacteria infections
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59.2%; Pred. No. 1.7e-90;
trive 50; Mismatches 75;
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                                The present sequence represents a protein encoded by open reading frame (ORF) D of a novel polymucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element, encode proteins which may be linked to pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium paratuberculosis and it has also been identified in Mycobacterium products of the intestine and Crohn's disease in humans. The protein products of the ORFs of GS can be used for detecting mycobacteria or for diagnosing, treating or preventing mycobacterial disease. In particular they can be used as vaccines for inflammatory diseases such as Crohn's disease or saccoidosis in humans or Johne's disease in animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli GDP-fucose synthetase.
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            Page 48; 62pp; English.
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The invention relates to a crystalline GDP-fucose synthetase (GFS). This was used to determine the crystal structure of GFS from Escherichia coli (AAY81360) to a resolution of 2.2 Angstroms. The structure of the enzyme when bound to its cofactor NADPH and product NADP+ has also been determined. The structure of GFS revealed it to be a member of the short chain dehydrogenase/reductase (SDR) family of enzymes which have a conserved core tertiary protein fold and a serine, tyrosine and lysine catalytic triad. GFS is particularly closely related to E. coli UDP-Galattic triad. GFS is particularly closely related to E. coli UDP-Galattic as a human catalytic triad as FX protein (AAY81351), which has 29% amino acid dentity. GDP-fucose is synthesised in a three-step reaction from GDP-mannose, with the second and third steps (epimerisation and GDP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose, with the second and third steps (epimerisation and COP-mannose) is the sugar donor. In humans, a defect con GDP-mannose is not seeful for identifying its agonists and antagonists and is useful for the design of immunosuppressants that act copy by blocking selectin mediated cell adhesion. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGSGOEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.3%; Score 943.5; DB 2 57.6%; Pred. No. 9.8e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY29659 standard; protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4; 56pp; English
                                                                (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.6
Matches 179; Conservative
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                                                                                                                                       Stahl ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: |: |: |:|
LASTYQWFLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 AA;
13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
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AAY29659
ID AAY29
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MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADAC--
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99US-0125054
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                                                                                                                                               298 LSQTYDWYLKN 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Running JA,
                                                                                                                                                                    |: || |:|:|
305 LASTYQWFLEN
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N-PSDB; AAZ45316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1999;
18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                 AAY54115;
187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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ID AAY5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an expression vector comprising a promoter linked to a nucleic acid (1) that encodes a prokaryotic enzyme (II) having both epimerase and reductase activity, for the catalysis of conversion of GDP (guanosine diphosphate) 4-keto-6-deoxymannose (III) to GDP-fucose (IV), where the vector lacks an Escherichia coli wcal coding region. An expression vector is specifically claimed where (I) encodes Escherichia coli YEF B. The present sequence represents the E. coli YEF B protein. (II) is used for production of (IV) which is then used to prepare fucosylated oligosaccharides (A) by enzymatic fucosyl transfer, e.g. to modify oligosaccharide components of glycoproteins or glycolipids, such as insulin, human or bovine growth hormones, tissue plasminogen activator, interleukins and viral antigens, or chimeric products such as immunoglobulin derivatives. (A) are variously useful as the rappeutic and diagnostic agents and in foods. Combining two activities in a single enzyme simplifies the process, allowing efficient synthesis of complex fucosylated oligosaccharides in a single reaction vessel from readily available starting materials. The method is suitable for large scale synthesis, e.g. 0.2 kg bacches. (II) can be expressed efficiently in prokaryotic cells (contrast similar mammalian enzymes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                         Escherichia coli, YEF B; expression vector; enzymatic conversion; guanosine diphosphate-4-keto-6-deoxymannose; GDP-mannose; GDP-fucose; fucosylated oligosaccharide; enzymatic fucosyl transfer; glycoprotein; glycolipid; insulin; growth hormone; tissue plasminogen activator; interleukin; viral antigen; therapeutic; diagnosis; food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S RVFIAGHRGWVGSAIRRQLEQRGDVELVLRTRDELNLLDSRAVHDFFASERIDQVYLAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vector expressing an enzyme that converts guanosine diphosphate-4-keto-6-deoxymannose to GDP-fucose, used to prepare fucosylated oligosaccharides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.0%; Score 937.5; DB 36.9%; Pred. No. 4.1e-87 tive 58; Mismatches 6
                                                                      Escherichia coli YEF B amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 41; Page 77; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                   99US-0071076
98US-0071076
                                                                                                                                                                                                                                                                                                                                99WO-US00893
                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 AA;
                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                          (CYTE-) CYTEL
                                                                                                                                                                                                                                                        WO9936555-A1
                                                                                                                                                                                                                                                                                                                                15-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                     4-JAN-1999;
                                    03-NOV-1999
                                                                                                                                                                                                                                                                                            22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sjoberg ER;
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AAY29659;
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                                                                                                                                                                                                                                               :|:| : |||::||: :|||::|| 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDP-4-keto-6-deoxy-D-mannose epimerase/reductase; GDP-D-mannose; GDP-L-galactose; vitamin C; ascorbic acid; L-ascorbic acid; ascorbic acid pathway enzyme; hexokinase; glucose phosphate isomerase; phosphomannomutase; L-galactose dehydrogenase; phosphomannomutase; L-galactose dehydrogenase; GDP-D-mannose pytrophosphorylase; GDP-D-mannose:GDP-L-galactose epimerase; GDP-L-galactose phosphorylase; L-galactose-1-P-phosphatase; L-galactose phosphorylase; C-galactose-1-P-phosphatase; L-galactono-gamma-lactone dehydrogenase; ester.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a GDP-4-keto-6-deoxy-D-mannose epimerase/
                                                       238 IGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG
--VFLLDRYSGLEHVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of ascorbic acid or esters, using microorganisms or plants which have genetic modification in enzymes involved in the ascorbic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A GDP-4-keto-6-deoxy-D-mannose epimerase/reductase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burlingame RP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page 170-171; 187pp; English.
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KVGGILANSSYPADFIYENIMIEANVIHAAHKNNVNKLLFLGSSCIYPKLAHQPIMEDEL 126
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                                                                                                                                                                                                                                                                                                                                           LTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL 186
                                                                                                                                                                                                                                                                                                                                                                                                              MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDR-YS------GLEHVN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 IGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 LRRFHDAVENNSPNVVVWGSGTPKREFLHVDDDMASASIYVMEMPYDIWOKNTKVMLSHIN
                                                                                                                                                                                                        7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
 improves the specificity of methods for the detection and identification of O antigens, e.g. in testing food- or faecalderived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic B. coli strains that
                                                                                                                                                                       ę,
                                                                                                                                                                         74; Indels
                                                                                                                                     DB 20;
                                                                                                                                       Score 915.5; DB 2
Pred. No. 7.4e-85;
                                                                                                                                                                         50; Mismatches
                                                                      cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #18359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG18368 standard; Protein; 576
                                                                                                                                       55.6%;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                         Matches 178; Conservative
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LENTYNWFLEN
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N-PSDB; AAS82555.
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                       323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG18368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                    64
                                                                                        MRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADAC------VFLLDRYSGLEHVN
                                                                                                                                                                                                                                                                                                    LRRFHEATAQNAPDVVVWGSGTPMREFLHVDDMAAASIHVMELAHEVWLENTQPMLSHIN
                                                                                                                                                                                                                                                                                                                                           238 IGSGQEVTIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDG
                                                                      7 KIFVAGHRGLVGSAIVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA
                                                                                                                                                                                                        LTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPAL
                                                                                                                                       KVGGIHANNTYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of a protein encoded by an open treading frame (ORE8) of a gene cluster (see AAXOG749) involved in the biosynthesis of the Escherichia coli 0157 O antigen. The protein shows homology to the E. coli WcaG colanic acid capsule protein. The use of nucleic acids derived from assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within O antigen gene clusters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food, faeces or patient samples
     DB 21; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen; 0157 antigen; diarrhoea; haemorrhagic colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen pathway ORF8 protein product.
 57.0%; Score 937.5; DB :
ilarity 56.9%; Pred. No. 4.1e-87
Conservative 58; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW88319 standard; Protein; 323 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 8; 165pp; English.
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97AU-0006545
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LASTYQWFLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang L;
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-059669,
N-PSDB; AAX06749
Query Match
Best Local Simi:
Matches 177; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli 0157
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01-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1998
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AAW88319
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WO9850531-A1
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                                    Lerchl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                     Frank M,
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                   The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (C restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and confidential and or acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed appear application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VWGTGSPLREFLHVDDLADAC------VFLLDRYSGLEHVNIGSGQEVTIRELAELV 253
                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDP-4-keto-6-deoxy-D-mannose 3,5-epimerase-4-reductase cDNA sequence #97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAGIKTCQAYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPALMRRFHEAKVNGAEEVV
                                                                                                                                                                                                                                                                                                                                                                                                             23 RKLQEQGFTNLVLKTHAELDLTRQADVESFPSQEKPVYVILAAAKVGGIHANNTYPADFI
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moss; carbohydrate metabolism related protein; CMRP; sugar; cofactor; fine chemical production; carbohydrate; polysaccharide.
                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                        43.7%; Score 718.5; DB 22; Length 576; 58.2%; Pred. No. 2.3e-64; ive 38; Mismatches 55; Indels 9;
                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
Claim 20; SEQ ID No 48727; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM00029 standard, Protein; 162 AA.
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                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.2%;
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                             576 AA;
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This invention relates to nucleic acid molecules AAH88796

isolated from Physcomitrella patens (a moss), which encode carbohydrate
metabolism related proteins (CMRP) represented in AAM0022 - AAM00110.

Corpubacian related proteins (CMRP) represented in AAM0022 - AAM00110.

Included in the invention is a vector containing the CMRP cDNA, and a
corpubacterium or Brevibacterium, moss or algae or a plant cell) is
corpubacterium or Brevibacterium, moss or algae or a plant cell) is
useful for producing a fine chemical such as carbohydrates, cofactors
and/or enzymes. The nucleic acid molecules are suitable for modifying a
carbohydrate production system in a host, e.g., microorganisms and
carbohydrate production system in a host, e.g., microorganisms and
carbohydrate production system in a host, e.g., microorganisms and
carbohydrate production system in a host, e.g., microorganisms and
carbohydrate production system in a host, e.g., microorganisms and
carbohydrate production system in a host, e.g., microorganisms and
cuther species which are useful to modify the biosynthesis of starch,
cell wall polysaccharides and sugars. The nucleic acid molecules may be
utilised in the genetic engineering of Corynebacterium and Chlorella to
make it a better or more efficient producer of one or more fine
chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs
chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs
chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs
chaving altered activities which indirectly impact the production of one
or more desired fine chemicals from plants. Primers AAH88705 - AAH80707
are used in the sequencing of the CMRP CDNA sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                             Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals such as carbohydrates, cofactors and enzymes from microorganisms and plants
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                                                                                  Bischoff F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 162;
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                                                                                      면, K
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                                                                             Cirpus Reski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.8%; Score 671; DB 22; 74.8%; Pred. No. 2.7e-60; ive 25; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O antigen; Olll antigen; wbdJ gene; diarrhoea;
haemorrhagic colltis; diagnosis.
                                                                             Reindl A, (
Schmidt R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 30; Page 114; 133pp; English.
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                                                                                  Ehrhardt T,
Duwenig E,
BADI ) BASF PLANT SCI GMBH.
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                                                                                                                                                                                                                 WPI; 2001-398155/42.
N-PSDB; AAH88715.
                                                                                      Renz A,
Freund A,
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61 LVGGIHANISRPFDFLEKNLQMGLNIVSVAKKLGIKKVLNLGSSCMYPKFEAIPEKAL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VIKKIHHAKINNVPEIEIWGDGNSRREFMYARDLADLIFYVIPKIEFMPNMVNAGLGYDY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 KVGGIHANNIYPADFIGVNLQIQTNVIHSAYEHGVKKLLFLGSSCIYPKFAPQPIPESAL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTASLEPTNEWYAIAKIAGIKTCQ-AYRIQHGWDAISGMPTNLYGPNDNFHPENSHVLPA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMRRFHEAKVNGAEEVVVWGTGSPLREFLHVDDLADACVFLLDRYSGLEH-VNIGSGQEV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 TIRELAELVKEVVGFEGKLGWDCTKPDGTPRKLMDSSKLASLGWTPKVSLRDGLSQTYDW 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 KIFVAGHRGLVGSALVRKLQEQGFTNLVLKTHAELDLTRQADVESFFSQEKPVYVILAAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KVLLTGSTGMVGKNILEHDSASKY-NILTPTSSDLNLLDKNEIEKFMLINMPDCIIHAAG 60
                                                                                                                                                                                                                                                                                                                                                                          This is the protein product of the wbdJ gene (ORF6) of a gene cluster (see AAX06748) involved in the biosynthesis of the Escherichia coli oll o antigen. It has high amino acid identity with the wead gene product and is likely to have a function in the antigen sugar biosynthetic pathway. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in testing food or faecal-derived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhagic colitis.
                                                                                                                                                                                                                                                       Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food faeces or patient samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.1%; Score 593.5; DB 20; Best Local Similarity 39.8%; Pred. No. 5.6e-52; Matches 121; Conservative 64; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 7; 165pp; English.
                                                      97AU-0008162
                98WO-AU00315
                                                                                                                                                                                               WPI; 1999-059669/05.
N-PSDB; AAX06748.
                                                                                                                  (UNSY ) UNIV SYDNEY
                                                                                                                                                          Wang L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AA;
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                                                      22-JUL-1997;
01-MAY-1997;
                                                                                                                                                          Reeves PR,
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			35 246.8 36 241.2 37 246.8 38 241.2 39 240.2 41 230.3 42 235.8 44 228.6 45 228.6		AUTHORS SEKI AUTHORS SEKI AUTHORS SEKI I toh TITLE Large JOURNAL Unpul COMMENT CONT. Plant RIKEL
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compu nucleic search, using sw model June 3, 2003, 02:39:05 ; Search t	US-10-089-014-2 936 1 atgtctgacaaatctgccaatg IDENTITY_NUC Gapop 10.0 , Gapext 1.0 ,	f hits satisfying chosen parameters length: 0 length: 2000000000 g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		12: 9D_est3:* 13: 9D_est4:* 15: em_estf6* 16: em_est6* 16: em_est6* 18: em_gss_hum:* 20: em_gss_hum:* 21: em_gss_hum:* 22: em_gss_hum:* 23: em_gss_hum:* 24: em_gss_hum:* 25: em_gss_hum:* 27: em_gss_hum:* 27: em_gss_hum:* 28: em_gss_hum:* 29: em_gss_hum:* 27: em_gss_hum:* 27: em_gss_hus:* 27: em_gss_hus:* 27: em_gss_hus:* 27: em_gss_hus:*	umber of or equal analysis analysis ngth DB 627 9 537 17 441 17 856 12 852 12
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F20D2TF IGF Arabidopsis thaliana genomic clone F20D2, DNA sequence. B22510 B22510. GI:2508240 GSS.
                                                                                   : - Centre National de Sequencage : (E-mail : seqref@genoscope.cns.fr
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 441)
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Pred. No. 3.9e-140;
0; Mismatches 0;
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                                                               Direct Submission
Submitted (25-UN-1999) Genoscope
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- Web : www.genoscope.cns.fr)
Location/Qualifiers
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/db xref="taxon:3702"
/clone="F8H3"
/clone lib="IGF"
/note="end : T7"
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     Samson, D., &
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and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS00P9U 537 bp DNA linear GSS 28-JUN-1999 Arabidopsis thaliana genome survey sequence T7 end of BAC F8H3 of IGF library from strain Columbia of Arabidopsis thaliana, genomic
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 537)
Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P.,
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/organism="Arabidopsis thaliana"
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/clone="RAFL16-16-116"
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                                                                                   Location/Qualifiers
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Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Coffey, E., Gol
, Johnson, K., Adams, M.D. and Venter, J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps
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                                                                                 Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tal: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Seq primer: M13-21
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Pred. No. 1.6e-117;
                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
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/b_xref="taxon:3702"
/clone="F20D2"
/clone_lib="IGF"
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Unpublished (1997)
Other_GSSs: F20D2TR
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Streptophyta; Embryophyta; Tracheophyta;
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/clone="cah_Ebb092C16f"
/clone lib="dosspoinm arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
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217 c 208 g 217 t 1 others
                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                           1 (bases 1 to 856)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
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Pred. No. 6.4e-112;
0; Mismatches 238;
                                                                                                                                                                                        Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: TAATACGATTCACTATAGGG
High quality sequence stop: 712.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gossypium arboreum"
/strain="AKA"
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Eukaryota; Viridiplantae;
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Email: dcook@ppserver.tamu.edu
Other name: Soybean RFLP probe; date: 4/20/99; Submitted to the
Database of Genome Survey Sequences (GSS) on 09/27/99; DNA sequence
of Soybean RFLP probe A890. Clones were obtained from Biogenetic
Services, Inc. More information is available at
'http://chrysie.tamu.edu/medicago'.
Seq primer: T3 (AATTAACCTCACTAAAGGG)
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Soybean RFLP probe Glycine max genomic clone A890, DNA
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The Crop Biotechnology Center
Texas A&M University
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Peterson Bldg, College Station, TX 77843-2132, USA
Tel: 409 845 8743
Fax: 409 862 4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Soybean RFLP probe"
/note="Vector: pBS+; Site_1: PstI; Site_2: PstI"
123 c 164 g 170 t
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Analysis of soybean RFLP probes
Unpublished (1999)
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llarity 76.5%; Pred. No. 1.3e-102;
Conservative 0; Mismatches 145;
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/db_xref="taxon:3847"
/clone="A890"
                                                                                                                                                                                                                                                                                                CCTACAAATGGTACGTCGAGAATGT 476
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                                                                           /organism="Zea mays"
/db_xref="WaizeDB:638464"
/db_xref="WaizeDB:638464"
/db_xref="WaizeDB:6377"
/clone="PCOJ43177"
/clone="Prod177"
/lote="Maize Mapping Project/DuPont Cornsensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs; to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1400 CCGACAAGGACGCCAAGGTCTTCGTCGCCGGCCACCGGGCCTCGTCGGCTCCGCCATCG 1341
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Pred. No. 6e-109;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546
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                                                                                                                                                                                               GATACTTCCGCTAAGATCTTCGTCGCCGGCCACCGTGGACTCGGATCCGCCGTGGTT
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                                                                                                                                                                                                                                                                                                                                                               CTAGCAGCAGCTAAAGTTGGTGGTATTCACGCTAACAACACCTATCCTGCTGATTTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH173899 731 bp DNA linear GSS 09-OCT-B216/R RFLP clone from soybean genomic DNA Glycine max genomic clone pB216 R primer, DNA sequence.
                                                                                                                                                                 ATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCAATCTCT
                                                                                                                                  Gaps
 acid, BTH, jasmonic acid, ethylene, fenthion, BIX, okadatc acid, or systemin prior to tissue harvest. site was destroyed during cloning."
                                                                                                                               .,
                                                                                                Length
                                                                                              Score 354.8; DB 10; Length
Pred. No. 2.1e-93;
0; Mismatches 182; Indels
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Grant, D. and Shoemaker, R.C.
unpublished sequence of soybean RFLP
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:15989266
                                                                                                37.9%;
71.8%;
                                                                                             Query Match
Best Local Similarity 71.8
Matches 464; Conservative
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA linear EST 18-MAY-2001
BTI Lycopersicon esculentum cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon.

1 (bases 1 to 652)

1 Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Pujii,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Bukaryora, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae, Solanum;
                                                                                                                               TCTCTATGGTCCTAATGACAATTTCCACCGGAGAATTCTCATGTGCTTCCTGCTCTTAT
                      TACTGGACCCTTAGAGCCCACAAATGAATGGTATGCCATTGCCAAGATTGCTGGGATCAA
                                                                GACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCAATCTCTGGCATGCCTAAA
                                                                                   CTTATATGGACCATATGACAATTTTCATCCCGAGAATTCGCATGTGTTACCTGCTCTCAT
                                                                                                                                                                                             GAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGTGGTGTGGGGTACAGG
                                                                                                                                                                                                                                                                               GGATCGATACAGCGGGTTGGAGCATGTTAACATTGGAAGTGGTCAAGAAGTGACTATTAG
AACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCTAAGATCGCTGGGATTAA
                                                                                                                                                                                                                               TAGTCCGTTGAGGGAGTTCTTGCATGTTGATGATTTGGCTGATGCTTGTGTTTTTCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Rio Grande ptoR"
/db_xref="taxon:4081"
/clone="clETBAS"
/clone=lib="tomato mixed elicitor, B:
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRP'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of ESTs from tomato leaf tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW041037
EST283901 tomato mixed elicitor, clone cLET8A5, mRNA sequence.
AW041037 GI:5899791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Lycopersicon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prime sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 TACTAAGCCTGATGGGAC
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SOURCE
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JOURNAL
COMMENT
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AUTHORS
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AW041037
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                  GSS 09-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:3847" /dlone="pa890" /clone="pa890" /clone lib="RFLP clone from soybean genomic DNA" /clone lib="RFLP clone from soybean genomic DNA" /note="Vector: pB85; PstI-generated fragments of genomic DNA. Library construction described by Keim, P. & Shoemaker, K.C. (1988) Soybean Gen. News. 15:147-148."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 TGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCTAAGATCGCTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 TCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGTGTGAAGAAGCTTCTCT
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                                                                                                                                max genomic
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                                                                                                  linear
DNA Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 566)
Grant, D. and Shoemaker, R.C.
unpublished sequence of soybean RFLP probe
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Grant D
Agronomy Department
USDA-ARS and Iowa State University
G304 Agronomy Hall, Ames, IA 50011-1010,
Tel: 515 294 1205
Fax: 515 294 2299
                                                                                 A890/R RFLP clone from soybean genomic clone pA890 R primer, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: dgrant@iastate.edu
single pass sequence
Class: RFLP clone.
                                                                                                                                                                                                                            GI:15989207
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Best Local Similarity 76.5%;
Matches 432; Conservative
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GSS.
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| organism="Glycine max" |
| db xref="pB216" |
| clone="pB216" |
| clone="pB216" |
| force="Vector: pB8+; PstI-generated fragments of genom: ONA. Library construction described by Keim, P. & Shoemaker, R.C. (1988) Soybean Gen. News. 15:147-148.
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                       Agronomy Department USDA-ARS and Iowa State University USDA-ARS and Iowa State University G304 Agronomy Hall, Ames, IA 50011-1010, USA Tel: 515 294 1205
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BG440809
GA Ea0010D16f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0010D16f, mRNA sequence.
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                                         215 CTCGCCGCCGCGAAGGTCGGCGCATACACGCAAACAATACTTACCCAGCTGATTTCATC 274
                                                                                                                                                                                                                                           335 AAGCTICTCTTCGTTCTTCATGTATTTACCCTAAATTTGCTCCTCAACCAATTCCC 394
                                                                                                                                                                                                                                                                                       GAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCTAAG 426
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Malvales, Malvaceae, Gossypium.
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University Genomics SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666 TTGTGTTTTCTTGCTGGATCGATACAGCGGGTTGGAGCATGTTAACATTGGAAGTGG 722
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                                                                                                                                         275 ACTATAAATCTTCAAATCCAAACAAACGTCATCGTTTCATCCTTCAATCACAAAGTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAATGCCCACGAATTTATATGGTACGAATGACCATTTCCATCCTGAGAATTCTCATGTT
                                                                                                  247 GGTGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGTGTGAAG
                                                                                                                                                                                            307 AAGCTTCTTCCTTGGATCATCCTGCATTTACCCTAAATTTGCTCCTCAGCCAATTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                              455 ATTGCTGGTATCAAATGTGTCTCAAGCTTATAGATTGCAGCATAACTTTGATGCAATTTCA

    687
    organism="Gossypium arboreum"

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Seg primer: TAATACGACTACATAGGG
High quality sequence stop: 683.
Location/Qualifiers
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/db xref="taxon:4113"
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/note="Vector: pBluescript of untreated and Phytophthora
infestans=treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
, tubers, or roots:"
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EST601830 mixed potato tissues Solanum tuberosum cDNA clone STMDG80
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1 (Dases 1 to 752)

Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Apr 17, 2002 this sequence version replaced gi:20168216.
CCGGAAGTCCATTGAGGGAGTTCTTGCACGTTGACGATTTGGCAGACGCGGTTGTTTA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contact the
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                                                                                                    481 TGATGGAAAAGTATAGCGGACTGGAGCATTTGAATGTAGGGGGTGGAAAGGAGGTTACTA
                                                                         TGCTGGATCGATACAGCGGGTTGGAGCATGTTAACATTGGAAGTGGTCAAGAAGTGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 GACAAAICIGCCAAAAICIICGICGCGGGICAICGIGGIIIGGAICIGCCAIIGIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato@tigr.org
This clone is available through the Research Genetics, conto Research Genetics for further information 1-800-711-6195 or conageresgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
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69.9%; Pred. No. 4e-92;
tive 0; Mismatches 214;
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/organism="Solanum tuberosum"
                                                                                                                                                                                               TTAAGGAATTGGCTGAGTTGATGAA 565
                                                                                                                                                                    TTAGAGAGTTGGCTGAGTTGGTGAA 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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BQ116267
BQ116267.2 GI:21917394
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Solanum tuberosum
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,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley, S.D. and Giovannoni,J.
Generation of BSTs from tomato carpel tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAGCTTGATCTCACT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 GCGGCGAAAGTCGGCGGCATACACGCAAACAATACTTACCCCAGCTGATTTCATCACATA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 AATCTGCAAATCCAAACGAACGTTATCGTTTCATCCTTCAATCACAAAGTTCAGAAGCTT 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 GCAGCTAAAGTTGGTGGTATTCACGCTAACAACACCCTATCCTGCTGATTTCATTGGTGTC
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                                                                             Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189

    614
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EST266954 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLED27F14, mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
, Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
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                                                       /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI'
213 c 134 g 173 t
  /tissue_type="Fibers isolated from bolls harvested
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                                                                                                                                        687;
                                                                                                                                    Score 339.8; DB 12; Length Pred. No. 5.7e-89; 0; Mismatches 167; Indels
                                          coli"
                    dpa"
/lab_host="E.
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AI897511.1 GI:5603413
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larity 72.5%;
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590 bp mRNA linear EST 18-MAY-2001 EST445993 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED13M21, mRNA sequence.
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Alcala,J., Visbalov,J., White,R., Matern,A.L., Vision,T., Holt,I.B.
Alcala,J., Edang,F., Vebalov,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Givannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
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/dev stage="5 days pre-anthesis to 5 days post-anthesis"
/dev stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_nost="XL1-Blue NRF"
/lab_nost="Vector: pBlueScript 6K(-); Site 1: EcoR1; Site 2:
Xho1; cLED - Tomato Carpel EST Library. OligodT-primed and
directionally cloned cDNA in vector Lamda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
and 1' ends located at the EcoRI and XhoI sites,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
      414 TCCCTGAAAATGCGCTCTTATCCGGTCCCCTGGAACCCACCAACGAATGGTATGCCGTTG 473
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                                                                       CTAAGATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCAA
                                                                                                                                    474 CCAAGATCGCGGGGATCAAAATGTGCCAAGCGTACAGAATTCAGCACGGCTTCGATGCTA
                                                                                                                                                                                                                                                                                                                                     ATGTGCTTCCTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGGAATGGAGCGGAGGAAG
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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Pred. No. 8.1e-84;
); Mismatches 158; Indels 0
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/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db xref="taxon:4081"
/clone="CLED13M21"
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Best Local Similarity 72.5%; Pre
Matches 417; Conservative 0;
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E (bases I to 664)

S Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.

ESTS from developing cotton fiber
Unpublished (1999)

Contact: Ben Burr
Biology Department
Brockhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnluxl.bnl.gov
                                                                                                                                                     MRNA linear EST 11-JUN-1999 BNLGHi6903 Six-day Cotton fiber Gossphium hirsutum cDNA 5' similar to (AF045286) GDP-4-keto-6-deoxy-D-mannose-3 5-epimerase-4-reductase [Arabidopsis thaliana], mRNA sequence. A1726948.1 GI:5045800
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| clone lib="Six-day Cotton fiber"
| rissue_type="lumature fiber"
| dev_stage="Six days post anthesis"
| lab_host="XL1.Blue"
| lab_nost="XL1.Blue"
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34.8%; Score 326; DB 9; L.
al Similarity 71.7%; Pred. No. 6.6e-85;
439; Conservative 0; Mismatches 172;
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65 CITTACCAATTAGGCTGCACAAATCTCATCCTCCGTACACATTCCGATCTCGATCTCACT 124
                                      133 CGTCAAGCCGATGTTGAATCCTTTTTTTCAAGAGAAGCCAGTTTATGTAATCCTAGCA 192
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US-08-322-463-14
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US-09-97-467-11
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Sequence 2, Application US/09103840A

Seneral No. 6294328

GENERAL INCPRARATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DNA SEQUENCES
FILE REFERENCE: 24366-2000/0.00

CURRENT APPLICATION NUMBER: US/09/103,840A

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATCHIN VOW. 2.1

SEQ ID NOS: 2

SEQ ID NO 2.2
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56.3%; Pred. No. 1.4e-81;
iive 0; Mismatches 402;
US-08-349-867-22
US-08-349-867-26
US-08-239-476-22
US-08-598-305A-22
US-08-598-305A-22
US-08-639-923A-26
US-08-639-923A-26
PCT-US95-05431-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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Matches 518; Conservative
   Similarity
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APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Bilault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
TITLE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN OF: 2.0
                                             GCGCCTGCTGCTCCTGGGCTCGTCGTGCATCTACCCGAAACTCGCCCCGCAGCCGATCCC
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Pred. No. 1.1e-82;
0; Mismatches 403;
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; ORGANISM: Mycobacterium tuberculosis
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Patent No. 6183957
GENERAL INFORMATION:
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Best Local Similarity 56.2%;
Matches 517; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGTTGAATCCTTCTTTTCTCAAGAGAGAGCCAGTTTATGTAATCCTAGCAGCAGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                               coli 0157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               6365723el Sequences of E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 269.8; DB 4;
Pred. No. 8.3e-81;
0; Mismatches 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORD Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 60/110,955
PILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       1705020 Gécerécráriceceáceace 1705039
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                                                                                                                                                                                                                                       US-09-453-702B-121/c

Sequence 121, Application US/09453702B

Patent No. 6365723

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (608) 251-5000
                                                                                                              TGATTGGTATTTGAAGAATG 925
                                                                                                                                                                                                                                                                                                                                        Burland,
Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                        Welch, Rod TITLE OF INVENTION: No. 6 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.8%;
.larity 57.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Madison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-453-702B-121
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Best Local S:
Matches 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 GAAGCTICICTICCTIGGAICAICCIGCATITACCCIAAAITIGCICCICAGCCAAITIC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                786 GCTTGGATGGGATTGCACTAAGCCAGATGGCACACCCGAGGAAACTTATGGACAGCTCAAA 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 GCTTCCTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCACTCGTCAAGCCGATGTTGAATCCTTCTTTTCTCAAGAGGCCAGTTTATGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 TGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1704480 GGAGAGCGCCTGCTCACCGGTCCGTTGGAGCCGACCAACGACGCGTACGCGATCGCCAA
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  FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                               Length 4411529;
                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 403;
                                                                                                                                                                                                                                                                                                          Score 275.2; DB
Pred. No. 5e-81;
                                       FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                              TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHEN INFORMATION: H37Rv US-09-103-640A-1
TITLE OF INVENTION: DNA SEQUENCES TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                          29.4%;
ilarity 56.2%;
Conservative
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 517; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTATTGCTAAGATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 GATGCAATCTCTGGCATGCCTACTAATCTCTATGGTCCTAATGACAATTTCCACCCGGAG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 aattatatagcagreatgccaaccaaccigraccccaaccaaccaacaatriccatriccaac

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 AATTCTCATGTGCTTCCTGCTCTTATGAGGAGGTTCCACGAGGC 578
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Pred. No. 3.2e-26;
; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 CACGGTGTGAAGAAGCTTCTCTTCCTTGGATCATCCTGCA
FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PORYPHYROMONAS GINGIVALIS
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Patent No. 593243
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          866:
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                     PP2911
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                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP291
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/1
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 429 base pairs
nucleic acid
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Best Local Similarity 60.9
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
                                   CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650-494-0792
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TELEFAX: 706141
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ORIGINAL SOURCE
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STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-221-017B-866
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                                   GITGGIGGIAITCACGCIAACAACACCIATCCIGCIGATITCATIGGIGICAAICICCAG 261
                                                                                                6194 GICGGAGGIATITIAGCIAACAGTICTIATCCIGCCGATITITATATATGAGAATATAATG
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Patent NO. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSER: MORISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                    ATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGTGTGAAGAAGC
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: DB COMPATER:
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US-09-221-017B-866
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                                                       GTGCTTCCTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGTT
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%30-221-017B-669, Application US/09221017B

%30-221-017B-669/C

%30-22
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FILING DATE: 23-DEC-1998
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MONITOY, Gladys H
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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TYPE: nucleic acid
STRANDEDNESS: double
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 ATCCATCTTGCTGCAATGGTGGGGGCCTGTTCCGGAATATCAAATACAATTTGGACTTC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 ATTGGTGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGTGTG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 AAGAAGCTTCTTCCTTGCATCATCCTGCATTTACCCTAAATTTGCTCCTCAGCCAATT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403 CGCAAGGTGGTGTCCTGCCTGTCCACCTGTATCTTCCCTGACAAGACGACTACCCGATA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 CCTGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 garicadaccangariccacaargescereceaeaeaeaeaeahrrregeraeeerargee 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 AAGATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCAATC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 AAGAGGATGATCGACGTGCAGAACAGGGCCTACTTCCAGCAGTACGGCTGCACCTTCACC 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 TCTGGCATGCCTACTAATCTCTAATGGTCCTAATGACAATTTCCACCCGGAGAATTCTCAT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 AICCTAGCAGCAGCTAAAGTTGGTGGTATTCACGCTAACAACACCTATCCTGCTGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,972
FILLING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 103.2;
Pred. No. 8.4
                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0400 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTR:
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: DOSA
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVANTION: ANTIGENS
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 48.9%;
Matches 341; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1352 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650-855-05
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LIBRARY: BLADNOT04
; CLONE: 1318190
US-08-937-972-4
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612 GGGTACAGGTAGTCCGTTGAGGGAGTTCTTGCATGTTGATGATTTGGCTGATGCTTGTGT 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          792 ATGGGATTGCACTAAGCCAGATGGCACACCGAGGAAACTTATGGACAGCTCAAAGCTCGC 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             852 GTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGCCAAACTTATGATTG 911
                                                                                                                                                                                                         552 TCCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGTGGTGTG
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                                                                                                                            DB 1; Length 7218;
                                                                                                                            Query Match
4.4%; Score 41.4; DB 1; Length 7;
Best Local Similarity 2.3%; Pred. No. 0.0026;
Matches 9; Conservative 214; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       912 GTATTTGAAGAATGTTTGCAACC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-232-463-14; Sequence 14, Application US/08232463; Patent No. 5670367; BELENEAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
    STRANDEDNESS: single
                       TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC (OPERATING SYSTEM:
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                                                                                   US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                     763 GAGGTIGITITGAAGGGAAGCTIGGAIGGGATIGCACTAAGCCAGAIGGCACACCG 822
                                                                                                                                                                                                                                                                                                                                                                                                                                       823 AGGAAACTTATGGACAGCTCAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTT 882
                                                                                                                                                                                                                                                                        703 CATGTTAACATTGGAAGTGGTCAAGAAGTGACTATTAGAGAGTTGGCTGAGTTGGTGAAA
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                        Length 517;
                                                                                                                                                                                                                               0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      883 AGAGATGGTCTGAGCCAAACTTATGATTGGTATTTGAAGAA 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 ACCACAGGIGIACGAATGTTAGTGGAITGGIAICGTCCGAA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
APPLICANT: SCHETFILINGER, F.
APPLICANT: FALIGNER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                    Query Match 5.8%; Score 54.6; DB 4; Best Local Similarity 52.9%; Pred. No. 1.5e-08; Matches 117; Conservative 0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FTLING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELEFRENCE/DOCKET NUMBER: 3472/114 IMMU
TELEPHONE: (703)836-9300
TELEFAX: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                          ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                MAME/KEY: misc_feature;
; LOCATION: 1...517
US-09-221-017B-669
                     UNKINOMIN
HYPOTHETICAL: NO
                   ANTI-SENSE: UNK
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-232-463-14/C
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                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GTTGAATCCTTCTTTTCTCAAGAGAAGCCAGTTTATGTAATCCTAGCAGCAGCTAAAGTT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 GGTGGTATTCACGCTAACAACACCTATCCTGCTGATTTCATTGGTGTCAATCTCCAGATT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 CAGACCAATGTGATCCACTCTGCATATGAGCACGGTGTGAAGAAGAGCTTCTTTCCTTGGA 324
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                                                                                                                                                                                                                                                                                                                                                                        25 ITCGTCGCGGGTCATCGTGGTTTGGTTGGATCTGCCATTGTCCGCAAGCTTCAGGAACAA 84
                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1426 YYYYYYYYGTACCAAATTCTTCTATCTTTAACTACTTGCATAGATAGG 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stassi, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiacan
APPLICANT: Read-Lopez, Ana
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Pereda-Lopez, Ana
APPLICANT: ARAXAS, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES, 34
ADDRESSE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 GCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCTAAGATCGCTGGG
                                                                                                                                                                                                                                                                                          Query Match
4.2%; Score 39; DB 1; Length 721
Best Local Similarity 5.1%; Pred. No. 0.017;
Matches 21; Conservative 210; Mismatches 180; Indels
  30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08858003
Patent No. 6060234
                                                                         TELEX: 899149
INFORMATION FOR ED ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
REFERENCE/DOCKET NUMBER: 3C
TELECOMMUNICATION INFORMATION
TELEPANE: (703)836-9300
TELEPAX: (703)683-4109
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                         US-08-232-463-14
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573 CGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGTGGTGTGGGGGTACAGGTAGTCCGTTGAG 632
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APPLICANT: Ruan, Xiaoan
APPLICANT: Recal-Lopez, Ana
APPLICANT: Rakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
WUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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Pred. No. 0.029;
0; Mismatches 119; Indels
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         MBER: US/08/858,003
16-MAY-1979
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Katz, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
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                                                                                                                                                                                                                                                                           FILING DATE:
THORREY AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
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TELECOMMUNICATION INFORMATION
TELEPHONE: (847)-938-3137
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Abbott Park
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IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 47.69
Matches 108; Conservative
DATA
                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
CURRENT APPLICATION DA APPLICATION NUMBER:
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573 CGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGTGGTGGGGGTACAGGTAGTCGTTGAG 632
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 36.6; DB 4; Length 925;
Pred. No. 0.029;
0; Mismatches 119; Indels
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NVENTION: 186 Human Secreted proteins
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
                                                                                                              4952.US.P2
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FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
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APPLICATION NUMBER: 60/040,333
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FILING DATE: 1997-03-07
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Patent No. 6420526
08/858,003
                  FILING DATE: 16-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
                                                                                                         REFERENCE/DOCKET NUMBER: 4
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Best Local Similarity 47.6%;
Matches 108; Conservative (
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                                                                                                                                                        TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
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                                                                                                                                                                                                   INPORMATION: OR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 925 base pairs TYPE: nucleic acid STRANBEDNESS: double TOPOLOGY: linear
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  APPLICATION NUMBER:
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TITLE OF INVENTION:
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APPLICANT: Stassi, Diane L.
APPLICANT: Stassi, Diane L.
APPLICANT: Ruan, Xiaoan
APPLICANT: Ruan, Xiaoan
APPLICANT: Reada-Lopez, Ana
APPLICANT: Rakavas, Stephan J.
APPLICANT: ARAKAVAS, Stephan J.
APPLICANT: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: NOVEL POLYKETIDE PRIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%; Score 36.6; DB 3; Length 925; Best Local Similarity 47.6%; Pred. No. 0.029; Matches 108; Conservative 0; Mismatches 119; Indels
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                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
MAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELECHONE: (847)-938-3137
TELEFRAX: (847)-938-2623
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,467
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08997467
Patent No. 6200813
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: DOS
FastSEQ Version 2.0
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  16-MAY-1979
                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott La
                                                                                                                                                                                                                                                                                                                                                                                                             linear
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OPERATING SYSTEM:
  FILING DATE:
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NUMBER: 60/047,633 1997-05-23 NUMBER: 60/047,583 1997-05-23 NUMBER: 60/047,617 1997-05-23 NUMBER: 60/047,618 1997-05-23 NUMBER: 60/047,503 1997-05-23 NUMBER: 60/047,503 1997-05-23 NUMBER: 60/047,592 NUMBER: 60/047,592 NUMBER: 60/047,593 NUMBER: 60/047,591 NUMBER: 60/047,581	997-05 98ER: 98ER: 98ER	1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0
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BARLIER FILING DATE: 1997-08-26
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EARLIER FILING DATE: 1997-08-27
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EARLIER PILING DATE: 1997-08-22
EARLIER APLICATION NUMBER: 60/056,892
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EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-23
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APPLICATION NUMBER: 60/047,615
PILING DATE: 1997-05-23
ADDITOT 1997-05-23
ADDITOT 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
                                                            APPLICATION NUMBER: 60/047,615
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,587
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,569
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
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                                                                                                                 R APPLICATION NUMBER: 60/056, 887
R FILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/056, 908
R APPLICATION NUMBER: 60/048, 964
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                                                       FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/056,909
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FILING DATE: 1997-08-22
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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Patent No. 6420526
GENERAL INFORMATION:
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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599

R APPLICATION NUMBER: 60/047,588

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,585

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,586

R APPLICATION NUMBER: 60/047,586

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A APPLICATION NUMBER: 60/056,894

R FILING DATE: 1997-08-22

A PPLICATION NUMBER: 60/056,911

R FILING DATE: 1997-08-22

A APPLICATION NUMBER: 60/056,636
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R APPLICATION NUMBER: 60/056,872

R FILING DATE: 1997-08-22

R PILING DATE: 1997-08-22

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,637
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,761
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APPLICATION NUMBER: 60/056,910
TILING DATE: 1997-08-22
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ICATION NUMBER: 60/043,576
                                                                                      APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,903
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
                                          APPLICATION NUMBER: 60/056,893
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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LICATION NUMBER: 60/047,501
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GENERAL INC. 0311423
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GENERAL INCOMMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MCLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00636
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT APPLICATION NUMBER: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36651 1071 geragcegaaereaaarreaerrrerereeaaeceeaeeareaeeeeaeaaan 1130 954 GATCTAGTGAATGGCCTCGTGGCTCTCATGAACAG---CAACGTCAGCAGCCCGGTCAAC 1010 CTTGCATGTTGAT 651 894 GGGGAGCCACTCACGGTATACGGATCCCGGGTCTCAGACAAGGGCGTTCCAGTACGTCAGC 953 772 GGTTTTGAAGGGAAGCTTGGATGGGATTGCACTAAGCCAGATGGCACACCGAGGAAACTT 831 712 ATTGGAAGTGGTCAAGAAGTGACTATTAGAGAGTTGGCTGAGTTGGTGAAAGAGGGTTGTT 652 GATTTGGCTGATGCTTGTGTTTTCTTGCTGGATCGATACAGCGGGTTGGAGCATGTTAAC Gaps ä, Length 2041; 3.7%; Score 34.8; DB 4; Length 20 48.8%; Pred. No. 0.2; tive 0; Mismatches 127; Indels 592 GCGGAGGAAGTTGTGGTGGGGTACAGGTAGTCCGTTGAGGGAGTT R APPLICATION NUMBER: 60/056, 862
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 887
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 908
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/048, 964
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-09-05
R APPLICATION NUMBER: 60/057, 650
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R APPLICATION NUMBER: 60/056,876
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,881
RR APPLICATION NUMBER: 60/056,909
RR APPLICATION NUMBER: 60/056,905
RR APPLICATION DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02 CATION NUMBER: 60/056,632 IG DATE: 1997-08-22 APPLICATION NUMBER: 60/056,664 Sequence 3, Application US/09738894A Patent No. 6331423 FILING DATE: 1997-08-22 1131 CCAGACATCAAAA 1144 832 ATGGACAGCTCAAA 845 Query Match 3.7 Best Local Similarity 48.8 Matches 124; Conservative RESULT 15 US-09-738-894A-3/c BARLIER PARLIER PARLIE g g 셤 셤 ò ò ઠ ð õ

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35539 TTATATTGTATCCCAAATATTTTTCGCAGCTGTAGAATTCTCACCTTGGCTGTGCTTT 35480
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Job time: 96 secs
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; ORGANISM: Human

; FEATURE:

; LOCATION: (1)...(36651)

; OTHER INFORMATION: n = A,T,C or G

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4-reductase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a GDP-4-keto-6-deoxy-D-mannose epimerase/ reductase. The enzyme catalyses the conversion of GDP-D-mannose to GDP-L-galactose. The enzyme can be modified, and used to produce transgenic microorganisms, which can be used in fermentation techniques to produce vitamin C (ascorbic acid, L-ascorbic acid). The enzyme is modified to increase its action. Other ascorbic acid) athway enzymes which may be used in the method of the invention include hexokinases, glucose phosphate isomerases, phosphomannose isomerases,
                                                                                                                                                     781 GGGAAGCTTGGATGGGATTGCACTAAGCCAGATGGCACACCGAGGAAACTTATGGACAGC
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"GDP-4-keto-6-deoxy-D-mannose epimerase/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                   The present invention provides the protein and coding sequences of the Arabidopsis thaliana GDP-4-keto-6-deoxy-D-mamnose-3,5-epimerase-4-reductase. The sequence can be used for the efficient production of GDP-1-fucose, which is essential to the production of functionally important sugar chains containing 1-fucose. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGTCCGCAAGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGATCTCACTCGTCAAGCCGATGTTGAATCCTTCTTTTCTCAAGAGAAGCCAGTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTAAGATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTCTGGCATGCCTACTAATCTCTATGGTCCTAATGACAATTTCCACCCGGAGAATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAATCCTAGCAGCAGCTAAAGTTGGTGGTATTCACGCTAACAACACCTATCCTGCTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                         Recombinant GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase derived from Arabidopsis for efficient production of GDP (guanine diphosphate)-L-fucose in vitro or in vitro
                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                         Length 936;
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                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 227 A; 190 C; 240 G; 279 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       Score 936; DB 22;
Pred. No. 3.1e-291;
0; Mismatches 0;
                                                                                                                                                                  Claim 3; Page 27-29; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 936; Conservative
                                      WPI; 2001-381292/40.
P-PSDB; AAG62614.
   Jigami
 Nakayama K,
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99US-0123180.
99US-0123548.
99US-0125788.
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                                                                                                            (first entry)
                                                                                                                                                                                                   Arabidopsis thaliana
                                                                   AAC34827 standard;
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
19-MAY-1999;
20-MAY-1999;
                                                                                                            17-OCT-2000
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23-MAR-1999;
25-MAR-1999;
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17-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                        EP1033405-A2
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23-APR-1999;
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27-MAY-1999;
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phosphomannomutases, GDP-D-mannose pyrophosphorylases, GDP-D-mannose:GDP-L-galactose epimerases, GDP-L-galactose phosphorylases, L-galactose dehydrogenases, and L-galactose-1-P-phosphatases, L-galactose dehydrogenases, and L-galactono-gamma-lactone dehydrogenases. The methods can be used for the production of ascorbic acid or esters using microorganisms or plants.
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                                                                                                                                               ATTGTCCGCAAGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAG
                                                                                                                                                                                        ATTGTCCGCAAGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAG
                                                                                                                                                                                                                      GTGAAGAAGCTTCTTCCTTGGATCATCCTGCATTTACCCTAAATTTGCTCCTCAGCCA
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                                                                                                                                  TTCATTGGTGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGT
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                                                                                                             Gaps
                                                                                                            12;
                                                                                       Length 1583;
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                                                                                                            Indels
                                                                Sequence 1583 BP; 407 A; 330 C; 351 G; 495 T; 0 other;
                                                                                      Score 857; DB 21;
Pred. No. 1.3e-265;
0; Mismatches 15;
                                                                                     Query Match 91.6%;
Best Local Similarity 97.1%;
Matches 918; Conservative
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Hybridisation assay, genetic mapping, gene expression control, protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
Arabidopsis thaliana DNA fragment SEQ ID NO: 8033
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Query Match 70.4%; Score 659; DB 21; Length 1353; Best Local Similarity 82.6%; Pred. No. 9.1e-202; Matches 766; Conservative 0; Mismatches 160; Indels 1.
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13-AUG-1999;
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Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals such as carbohydrates, cofactors and enzymes from microorganisms and plants

Claim 7; Page 104; 133pp; English.

Bischoff F;

면, K Cirpus Reski

Reindl A, Schmidt R,

Ehrhardt T, Duwenig E,

Freund A, 2001-398155/42

Lerchl J,

Frank M,

P-PSDB; AAM00095

Ehrhardt

14-DEC-2000; 2000WO-EP12697

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99US-0171101 SCI GMBH

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This invention relates to nucleic acid molecules AAH88796
isolated from Physcomitrella patens (a moss), which encode carbohydrate
metabolism related proteins (CMRP) represented in AAM0022 - AAM00110.
Continued in the invention is a vector containing the CMRP cDNA, and a
continued in the invention is a vector containing the CMRP cDNA, and a
correlation or Brevibacterium, moss or algae or a plant cell) is
correlated producing a fine chemical such as carbohydrates, cofactors
and/or enzymes. The nucleic acid molecules are suitable for modifying a
carbohydrate production system in a host, e.g. microorganisms and
carbohydrate production system in a host, e.g. microorganisms and
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carbohydrate production system in a host, e.g. microorganisms and
carbohydrate production system in a host, e.g. microorganisms and
carbohydrate production system in a host, e.g. microorganisms and
cuther species which are useful to modify the biosynthesis of starch,
cell wall polysaccharides and sugars. The nucleic acid molecules may be
cutilised in the genetic engineering of Corynebacter xylinum and the
contained in the sequencing of the CMRP cDNA sequences of the invention.

contained altered activities which indirectly impact the production of one
contained in the sequencing of the CMRP cDNA sequences of the invention.
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GAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATTGCTAAG 426

367

Physcomitrella patens

fine

WO200144476-A2

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Query Match
Best Local Similarity 58.2
Matches 522; Conservative
WPI; 1997-351061/32.
P-PSDB; AAW21771.
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                      GAGGAGTCGCTCCTGACAGGGCCTTTGGAAGCTACAAACGAGTGGTATGCTGTAGCAAAG
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                                                            ATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCAATCTCT
  Open reading frame D from the GS region of M. paratuberculosis.
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The present sequence represents one of eight open reading frames (ORFs) of a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element of 2.5 kb. The ORFs, and also pathogenecity, such as providing receptoris for cellular recognition. GS was discovered and characterised using differential DNA analysis also been identified in Mycobacterium paratuberculosis and it has also been identified in Mycobacterium avium subspecies silvaticum. These pathogenic mycobacteria cause chronic inflammation of the intestine and crohn's disease in humans. The protein products of the ORFs of GS can be mycobacterial mycobacterial or for diagnosing, treating or preventing mycobacterial or for diagnosing, treating or preventing inflammatory disease. In particular they can be used as vaccines for inflammatory disease such as Crohn's disease or sarcoidosis in humans or
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pathogenicity island from mycobacteria - used to cts for detection, diagnosis, prevention and treatment
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Pred. No. 5.1e-85;
0; Mismatches 375;
                                                                                                                                      Claim 6; Page 48; 62pp; English.
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                                                                                                        GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's dise vaccine; inflammatory disease; sarcoidosis; Johne's disease; ss.
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an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element, encode proteins which may be linked to pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium subspecies silvaticum. These pathogenic mycobacteria cause chronic inflammation of the intestine and Crohn's disease in humans. The protein products of the ORFs of GS can be used for detecting mycobacteria or for disagnosing, treating or preventing mycobacteria or for disagnosing, treating or preventing mycobacterial disease. In particular they can be used as vaccines for inflammatory diseases such as Crohn's disease or sarcoidosis in humans or
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Pred. No. 1.1e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents one of eight open reading frames (ORFs) of a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb off DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The ORFs, and also pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium paratuberculosis and it has also been identified in Mycobacterium paratuberculosis and it has pathogenic mycobacteria cause chronic inflammation of the intestine and used for detecting mycobacteria or for diagnosing, treating or perventing mycobacteria. They protein products of the ORFs of GS can be used for detecting mycobacterial or for diagnosing, treating or perventing mycobacterial in particular they can be used as vaccines for the language of the order of the control of the inflammator diseases un paratural they can be used as vaccines for the order of the o
                                                                                                                                                                                                                                                                                                                       GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease; vaccine; inflammatory disease; sarcoidosis; Johne's disease; ss.
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                                                                                                                                                                                                                                                                                    Open reading frame D from GS region of M. avium subspecies silvaticum.
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P-PSDB; AAW21770.
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TCACCAATCTCGTTCTTAAAACACACGCCGAGCTTGATCTCACTCGTCAAGCCGATGTTG
                                                                                                              164 TCACCAATCTCATTGTGCGATCACGCGATGAGATTGATCTGACGGACCGAGCCGCAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple open reading frames (ORFs) and an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element, encode proteins which may be linked to be pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium avium subspecies silvaticum and it has also been identified in Mycobacterium paratuberulosis. These pathogenic mycobacteria cause chronic inflammation of the intestine and crohn's disease in humans. The protein products of the ORFs of Gs can be used for detecting mycobacteria or for disgnosing, treating or preventing mycobacterial disease. In particular they can be used as vaccines for inflammatory diseases such as Grohn's disease or sarcoidosis in humans or Johne's disease in animals.
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velop products for detection, diagnosis, prevention and treatment
mycobacteria infections
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Sumar N,
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Best Local Similarity 58.1 Matches 521; Conservative

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                                                                                 1704729 Gecearecceáccaaccreraceseccaseceácaacrrrreseceresecresearer
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         TGGCATGCCTACTAATCTCTATGGTCCTAATGACAATTTCCACCCGGAGAATTCTCATGT
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen. Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAL199683) and H37Rv (AAL99682). The method is useful for evaluating strain variation of m. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
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using a bacterial artificial chromosome (BAC) vector. Recombinant BAC vectors, which are preferably immobilised, can be used to detect mycobacterial nucleic acids (genomic DMA, cDNA or mRNA) in biological samples. The polymucleotides identified are useful as probes or primers for detecting a given mycobacterium of interest. By aligning the polymucleotides identified are useful as probes or primers polymucleotides contained in the recombinant BAC vectors it is possible to physically map a polymucleotide of mycobacterial origin in a biological sample. The methods and vectors from the present invantion are useful in providing information for combating tuberculosis. It is possible to compare genomes between different strains or species and their non-pathogenic strains or species counterparts. ABQ62492 to ABQ6328 and ABB81230 represent sequences used in the exemplification of the present invention.
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                                                                    GCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGCCAAACTTA
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specifically claimed in Claim 6; e
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                                                                         /product= sugar_transferase
/note= "wobN gene (ORP1), this region is
specifically claimed in Claim 6;
AAW88312"
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/note= "wzy gene (ORP?), this region is
specifically claimed in Claim 6;
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'wzx gene (ORP4), this region is
specifically claimed in Claim 6,
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/note= "wbdo gene (ORF3), this region
specifically claimed in Claim
AAW88314"
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835 GACAGCTCAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTG 894
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                                                                           8227 ACTCCAAAGCGTGAATTCTTACATGTAGATGATATGGCTTCTGCAAGCATTTATGTCATG
                                                                                                                                                                                                                                                                    8287 GAGATGCCATACGATATATGGCAAAAAATACTAAAGTAATGTTGTCTCATATTT
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                                                                                                                          AGTCCGTTGAGGGAGTTCTTGCATGTTGATGATTTGGCTGATGCTTGTGTTTTTCTTGCTG
                                                                                                                                                                                                                    -----ATCGATACAGCGGGTTGGAGCATGTTAACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid molecule useful for the detection of flagellated
bacterial strains in food, faeces, etc.
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                              AGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGGGAAACTIGAGCCAACAATGAACCTIAIGCTAICGCAAAAATIGCAGGTAITAAA 8046
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                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence of a gene cluster involved in the biosynthesis of the Escherichia coli 0157 0 antigen. The gene cluster was obtained by PCR amplification of E. coli 0157:47 strain (C664-1992) DNA using primers (see AANG6752-63) based on 0 antigen gene sequences. 12 Open reading frames within the gene encode proteins (see AAN8313-23) involved the sequences. The genes encode proteins (see AAN8313-23) involved the synthesis of sugars present in the polysaccharide or oligosaccharide the transport or processing of polysaccharide or oligosaccharide units. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wad (transferase), wzx (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in tests of food- or faecaldentived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ATCTTCGTCGCGCGTCATCGTGGTTTGGTTCTGCCATTGTCCGCAAGCTTCAGGAA
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                                                                                                                   P-PSDB; AAW88312, AAW88313, AAW88314; AAW88315, AAW88316, AAW88317,
AAW88318, AAW88319, AAW88320, AAW88321, AAW88322, AAW88323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 14024;
                                                                                                                                                                                         Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14024 BP; 4546 A; 2263 C; 2832 G; 4383 T; 0 other;
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0; Mismatches 372;
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                                                                                                                                                                                                                                                                                          Claim 6; Fig 8; 165pp; English.
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(UNSY ) UNIV SYDNEY
                                                  Wang L;
                                                  Reeves PR,
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of E. coli of H serotype in a sample by hybridising at least one or a pair of (1) to any E. coli in the sample and detecting the hybridised nucleic acid molecules, and (2) for detecting the presence of both O and H-serotypes of E. coli by hybridising at least one or a pair of (1) to any E. coli present in the sample and detecting the hybridised nucleic acid molecules. (1) is particularly useful for detecting the combination of O and H antigen. Hybridised (1) when using at least one (1) is detected by southern blot analysa and, when using a least one is detected by polymerase chain reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                     GITGGTGGTATTCACGCTAACAACACCTATCCTGCTGATTTCATTGGTGTCAATCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                             GrcGGAGGTATTTTAGCTAACAGTTCTTATCCTGCCGATTTTTATATATGAGAATATAATG
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                                                                                                                                                                                                                             ATCTTCGTCGCGCGCTCATCGTGGTTTGGTTGGATCTGCCATTGTCCGCAAGCTTCAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 AGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGTGGTGTGGGGTACAGGT
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                                                                                                                                                                                                   27; Gaps
                                                                                                                                                                          DB 21; Length 14024;
                                                                                                                                               Sequence 14024 BP; 4546 A; 2263 C; 2832 G; 4383 T; 0 other;
                                                                                                                                                                        28.8%; Score 269.8; DB 21; Length 57.1%; Pred. No. 1.2e-75; indels ive 0; Mismatches 372; Indels
                                                                                                                                                                   Query Match
Best Local Similarity 57.1
Matches 530; Conservative
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                                            8467 GAIGIAACGCIICIICAICAACIAGGIIGGAAICAIAAAAIIACCCIICACAAGGGICII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ferandard_name= "ORF KS"
product= "aninotransfersse-like protein"
note= "homologous to the BioA gene"
14056..425594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard_name= "ORF K8"
product="glutamate dehydrogenase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "homologous to the GLUD1 gene"
complement (430538..431284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="oligopeptide permease"
/note= "homologous to the OppC gene"
418673..419680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product=""oligopeptide permease"
note= "homologous to the OppD gene"
19677..420738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "ORF K3"
/product= "oligopeptide permease"
/note= homologous to the OppF gene"
120774..422159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product=""encapsulation-like proteinote="homologous to the CapA gene' 22628. 424031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "transposase homologue"
complement (431296..432840)
/*+≈~- '
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/product=""transposase homologue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="transposase homolog
note= "homologous to the Tnp
128292..429623
                                                                                                                                               GAAAATACATACAACTGGTTTCTTGAAAA 8555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard_name= "ORF K1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              name= "ORF K9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard name= "ORF K4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         name= "ORF K7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard name= "ORF K2"
                                                                                                   895 AGCCAAACTTATGATTGGTATTTGAAGAA
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/standard_name= "QRF L2"
/product= "gamma-hexachlorocyclohexane-dechlorinase-like
protein"
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                                                                                                                                                                                                                                                                                                                                                      Product= "alpha-subunit of FeMo protein of nitrogenase"
54590..456131
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "beta-subunit of FeMo protein of nitrogenase"
456187..457677
                                                                                                       /*tag= z
/standard_name= "ORF L3"
/product= "putative protein with degradative function"
450341..451396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ATCTTCGTCGCGGGTCATCGTGGTTGGATCTGCCATTGTCCGCAAGCTTCAGGAA
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product= "protein similar to part of the Fe protein
                                                                                                                                                                                                           /standard_name= "ORF L4"
/product= "luciferase alpha-subunit-like protein"
//note= "homologous to the LuxA gene"
452980..454494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 534720;
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'product= "protein involved in FeMo co-factor
biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product=""protein involved in FeMo co-factor
biosyntheais"
/note= "homologous to the FixF gene"
459093..459575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "ORF L15"
/product= "processing protease-like protein"
/note= "homologous to the PP gene"
466590..467021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 28.3%; Score 265; DB 19; Length 5:
Local Similarity 56.6%; Pred. No. 3e-73;
1es 512; Conservative 0; Mismatches 390; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard_name= "ORF L11"
product= "protein of unknown function"
60501..460920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'standard name= "ORF L10"
'product=""protein of unknown function"
'note= "homologous to the NifX gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name= "ORF L13"
|product="mprotein of unknown function"
|63201..464739
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/product= "peptidase-like protein"
/note= "homologous to the bI-MPP gene"
464736..466079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // Anotes "homologous to the NifH gene" (18128..461545)
                                                                 /note= "homologous to the LinA gene" 448497..450203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "homologous to the NifB gene
                                                                                                                                                                                                                                                                                                                                                                                                     /scandard name= "ORF L7".
/gene= "nifk"
                                                                                                                                                                                                                                                                                           /*tag= ab
/standard_name= "ORF_L6"
/gene= "nifD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             name= "ORF L9"
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/standard_
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/standard:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene= "fixC"
/product= "protein required for nitrogenase activity"
complement (439923..441032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Product= "protein required for nitrogenase activity" complement (442316..442636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Product= "protein required for nitrogenase activity"
complement (441042..441899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product= "positive regulator of nif, fix and other
                                                                                                                                                                                                                           /*tag= m
/standard_name= "ORF K13"
/product= "ferrodoxin/ferrodoxin-like protein"
/note= "homologous to the FdxN gene"
complement (434753.,436234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "C4-dicarboxylate transport protein"
note= "homologous to the DctAI gene"
                                                                                                                                                                                                                                                                                                                                                                                          'product= "protein involved in FeMo co-factor
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/standard_name= "ORF L1"
/product="cytochrome P450-like protein"
/note= "homologous to the CamC gene"
447844..448500
                                                                                  function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard_name= "ORF K21"
|product="protein of unknown function"
|44337..445029
                                                                                                                                                              /standard_name= "ORF K12"
/product=""protein of unknown function"
complement (434517..434711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product=""protein of unknown function"
complement (443313..443879)
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145088..446602
                                                             /standard_name= "ORF K11"
/product= "protein of unknown functi
/note= "homologous to the FixU gene"
complement (434107.434433)
    /note= "homologous to the Tnp gene"
complement (433880..434110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'standard_name= "ORF K22"
'product="'ferrodoxin-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                               biosynthesis"
complement (436460..438130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (438297..438590)
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'gene= "nifB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _name= "ORF K16"
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'gene= "fixB"
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standard_name= "ORF K15"
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standard_name= "ORF K23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene= "fixA"
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/standard
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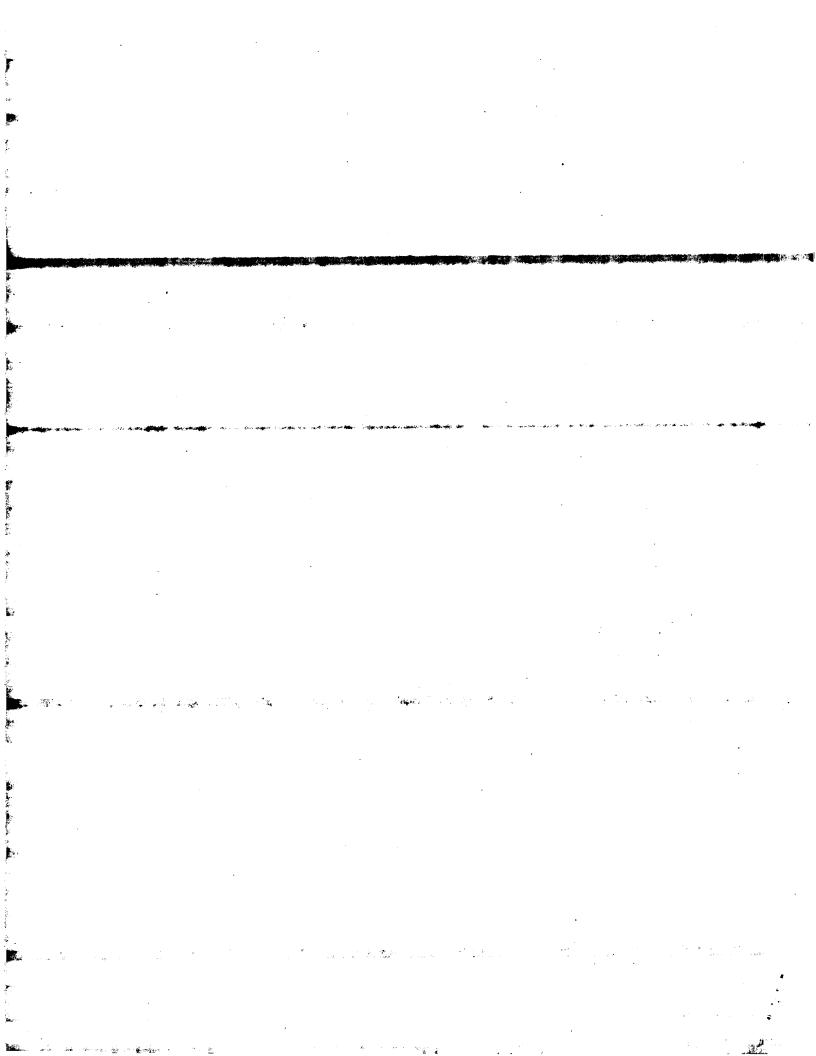
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Arabidopsis thaliana
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis. Arabidops Arabidops Arabidops AC025908 Arabidops AC034106 Sequence Sequence Arabidops Escherich AE000064 Rhizobium A79350 Sequence 1 A93002 Sequence 1 AR128139 Sequence complete score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AB034806 939 bp mRNA linear PLN Arabidopsis thaliana AtFX mRNA for GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase, AP002559 AB034806.1 GI:7804473 AB034806.1 GI:7804473 GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase. ALIGNMENTS SUMMARIES AP002559 AF285084S1 AE000064 MTCY277 YPE251713 YEU46859 AE007023 PBU42580 AX172657 AE013290 AE007718 MAP223833 MAS223832 AR128139 AE009407 DB 1490 10029 8458 1020 44435 1020 7995 8938 31.6 25861 31.6 71286 30.4 10999 30.4 20588 29.9 26913 29.4 12732 29.4 38300 29.3 20045 29.3 20045 29.0 20148 29.0 20148 28.9 12016 Length 12666 14002 14029 14187 320040 320040 130393 130393 130393 11429 31482 % Query Match 71.3 70.4 46.0 41.8 228.88.88.88 228.88.88.88 228.33.488.888 238.33.4888 275.2 275.2 275.2 274.2 271.8 271.8 270.2 269.8 667.8 667.8 667.8 667.8 659 354 RESULT 1 AB034806 LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE

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Arabidopsis thaliana.

Arabidopsis thaliana

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 939)

Bonin, C.P. and Reiter, W.D.

A bifunctional epimerase-reductase acts downstream of the MURI gene

product and completes the de novo synthesis of GDF-L-fucose in
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GDP-4-Keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GERI) gene, complete cds.
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Submitted (19-APR-2000) Molecular and Cell Biology, Univer
Connecticut, 75 North Eagleville Road, Storrs, CT 06269, U
Sequence update by submitter
On Apr 19, 2000 this sequence version replaced gi:6016478.
Location/Qualifiers
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Bonin,C.P., Potter,I., Vanzin,G.F. and Reiter,W.-D.
Direct Submission
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Nakayama, K. and Jigami, Y.
Direct Submission
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Submitted (09-NOV-1999) Ken-ichi Nakayama, National Institute of
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Nakayama,K., Maeda,Y., Wang,X. and Jigami,Y.
Expression of the genes for GDP-fucose synthesis in yeast
Saccharomyces cerevisiae
Unpublished
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/codon_start=1
/product="GDP-4-keto-6-deoxy-D-mannose-3,
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                                                                                                                                                                                Higashi, Tsukuba, Ibaraki 305-8566, Japan
(E-mail:nakayama@nibh.go.jp, Tel:81-298-54-6226,
Fax:81-298-54-6220)
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; Pred. No. 1.2e-265;
0; Mismatches 0;
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1. .939
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/db_xref="G1:7804474"
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Best Local Similarity 100.
Matches 936; Conservative
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Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CR-081.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, http://GR-081.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, http://www.tigr.org/softlab/glimmerm.htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/cgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Arabidopsis thaliana chromosome 1 BAC T18K17 genomic sequence
Unpublished
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T18K17 genomic sequence,
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The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                          841 TCAAAGCTCGCGTCTTTGGGTTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGCCAA
                                                                                                                                                                                                           GGGAAGCTTGGATGGATTGCACTAAGCCAGATGGCACACCCAGGAAACTTATGGACAGC
                                                                                                                                                                                                                                                                    TCAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGCCAA
                                                         GATGCTTGTGTTTTCTTGCTGGATCGATACAGCGGGTTGGAGCATGTTAACATTGGAAGT
                                                                                                    GGTCAAGAAGTGACTATTAGAGAGTTGGCTGAGTTGGTGAAAGAGGTTGTTGGTTTTGAA
                                                                                                                                        GGTCAAGAAGTGACTATAAGAGAGTTGGCTGAGTTGGTGAAAGAGGGTTGTTGGAAA
                                                                                                                                                                                   GGGAAGCTTGGATGGGATTGCACTAAGCCAGATGGCACACCGAGGAAACTTATGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdrown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280860. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Linyx. and Kaul,S.
Direct Submission
Submitted (15-SEP-1999) The Institute for Genomic Research,
Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 70836)
Town,C.D. and Kaul,S.
                                                                                                                                                                                                                                                                                                                                                                           901 ACTTATGATTGGTATTTGAAGAATGTTTGCAACCGA 936
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KLLFLGSSCIYPKFAPQPIPESALLTASLEPTNEWYAIAKIAGIKTCQAYRIQHGWDA
LADACVFLLYGPNDNFHPENSHYLPALMRRFHBAKVNGAEEVVVWGTGSBLREFLHVDD
LADACVFLLDRYSGLEHVNGSGQETVIRELAELVKEVVGFEGKLGWDCTKPDGTPRK
LMDSSKLASLGWPKYSLRDGLSQTYDWYLKNVCNR"

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                                                                                                  /gene="GER1"
/product="GDP-4-keto-6-deoxy-D-mannose-3,
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                                                                                                                                                                                                                                                                                 5-epimerase-4-reductase"
/protein_id="AAC02703.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
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                                                                               . >939
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Best Local Similarity 100.
Matches 936; Conservative
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join(12385. 12533,12631. 12776,12858. 12934,12999. 13121,
13208. 13310,13426. 13565,13643. 13729,13820. 13888,
13969. 14040,14131. 14249,14327. 14440,14520. 14565,
                                                                                                                                                                                                                           MKLDVYNGTLESLVSTTYSWYKTSSMIFLDOPVGTGFSYSRTQGFNKFSDSGEAKRIH
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/rpt family="(TA)n"
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VOGEVVIKBLCVTETPROYIYRYLLIYWWNDNYRALDINKESIGEWVRCYFGIPY
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DQIGGYTKTYANKWTFATVRASGHTAEYKPYETYIMPHRWINGOPL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="IIBKL7:4"
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/note="similar to serine carboxypeptidase I precursor
GB:P07519 [Hordeum vulgare], glucose acyltransferase
GB:AD01263 [Solanum berthaulti]; contains Pfam profile:
PF00450 Serine carboxypeptidase"
join(<8937. 9082,9167. 9312,9394. 9470,9553. 9675,
9780. 9882,9952. 10091,10176. 10256,10362. 10430,
10527. 10598,10670. 10788,10877. 10990,11097. 11146,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(8937. .9082,9167. .9312,9394. .9470,9553. .9675,
9780. .9882,9952. .10091,10176. .10256,10362. .10430,
10527. .10598110670. .10788,10877. .10990,11097. .11146,
11234. .11310)
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'db_xref="GI:12324329"
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/db_xref="GI:12324326"
note="contains non-consensus splice site"
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complement(11683. .11712)
/rpt_family="AT_rich"
complement(11785. .11807)
/rpt_family="AT_rich"
12385. .14737
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/rpt_family="(TA)n"
11537. .11568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to serine carboxypeptidase I precursor GB:P07519 [Hordeum vulgare], glucose acyltransferase GB:P07519 [Hordeum vulgare], glucose acyltransferase GB:AD01263 [Solanum berthaultii]; contains Pfam profile: Pr00450 Serine Sar. 2012, 2998. .3074,3151. .3273, 3377. .3459,3546. .3685,3762. .3848,3946. .4014,4096. .4167,4237. .4355,4441. .4554,4650. .4695,4812. .>4892) /gene="right"/">1010(2530. .2678,2770. .2915,2998. .3074,3151. .3273, 3157. .3459,3546. .3685,3762. .3848,3946. .4014,4096. .4167,4277. .4355,4441. .4554,4650. .4695,4812. .4892)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(5659. .5807,5899. .6044,6153. .6229,6315. .6437,
6527. .6629,6714. .6853,6937. .7023,7122. .7190,7278. .7349,
7429. .7547,7619. .7732,7814. .7859,7954. .8034)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFPASESESESESDLAAAEIMVIWAIQGPTSFAPNTLVAQSSLELRLDACGHSLSILQ
SPCSLANTPGYTGSWMDSQVLGKFEHSVDSKYLSLBGKKIVTBLGSCGLVGCIAAL
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VLEYFLETALKDFAIGRVEQTQWHPDYRSHRVVLYVLEKKKSKRCLADESSLNQSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MANNNVYSVLKSLLLLHLVFLSKQHVDSASIVKFLPGFEGPLP
FELETGYIGVGEEEEVQLFYYFIKSERNPKEDPLLLMLTGGPGCSAISGLLYQNGPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLTDCVYDCNYRVPFAHKMALISDELYESLKATCRGEYVNVHPHDTECLKFVEEFNKL
THRVCERFILHSCCETETSCYSYRFATTYWANDETVRKALQINKESIGEWTRCYRG
IPXNHDIKSSVPYHMINSIDGYRSLIYSGDHDIQVPFLATQAMIRSLAYSIIDDWRPW
MIKDQIAGYTTSYVNKYYFATVTGGGHTAEFTPKETFMMFQRMINGQPL"
                               tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
Simple repeats are identified by repeatmasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLDVYNGTLPSLVSTTYSMTKTSSMIFLDQPVGTGF8YSRTQLFNKPSDTGEARRIH
EFLQKWLGKHQEFSSNPFYVGGDSYSGLVVPATVQEISKGNCQCCNRPINLQGYVLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="pueative serine carboxypeptidase; 2530-4892"
/protein_id="AdG51126.1"
/db_xref="GI:12324317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(<516. .836,1121. .1263,1342. .1526,1807. .>1979)
gene="T18K17.1"
   proteins. Genes encoding tRNAs are predicted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(516. .836,1121. .1263,1342. .1526,1807. .1979)
/gene="T18K17.1"
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                                                                                                                                                                                                   organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (4703, .4758)
/rpt_family="(A)n"
5659. .8034
                                                                                                                                                                                                                           /cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                       complement (382. .402)
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/gene="T18K17.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="T18K17.3"
                                                                                                                                                                                                                                                                                                                                       /clone="T18K17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="T18K17.3
   hypothetical
                                                                                                                                                                                                                                                                                                                                                                          repeat_region
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Arabidopsis thaliana.

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1018)

Y amada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Cheng, J.M., Chodera, C.S., Quach, H.L., Tang, C., Toriuni, M., Wu, H.C., Yamamura, Y., Yu, G., Boweer, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Saki, M., Shinn, P., Southwick, A., Shinnozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A., Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                         1018 bp mRNA linear PLN 06-MAY-2002 thaliana putative GDP-L-fucose synthetase (At1g17890)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakural,T., Carninci,P., Kawai, J.,
Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1018)
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Carninci,P., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.
Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
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Location/Qualifiers
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/db_xref="GI:20465283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
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ecotype: Columbia"
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/gene="At1g17890"
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/gene="At1g17890"
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                                                                                                                                                                                                                     AY096364.1 GI:20465282
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AY096364
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                                                       RESULT 4
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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MKLDVYNGTLPSLVSTTYSWTKASSMIFLDQPVGAGFSYSRTQLLNKPSDSGEAKRIH
EFLQKWLGKHQEFSNPFTVGGDSYSGMVVPATVQBISKGNYBCCNPPINLGGYVLGN
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TNSICORRIIDPFGFTPTPNCYTKRFLLAAYRANDETVRKALQIKKETIGEWYKCHYG
IPYNYDIKSSIPYHMNNSINGYRSLIYSGDHDFEVPFLĞTQAMIRSLNYSVIDDWRPW
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                                                                                                                                                                                                                                                                                                                                                                           ATTIGTCCGCAAGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22276 GGTCAAGAAGTGACTATTAGAGAGTTGGCTGAGTTGGTGAAAGAGGGTTGTTGGAA
                                                                                                                                                                                                                                                                  21736 GTAATCCTAGCAGCAGCTAAAGTTGGTGGTATTCACGCTAACAACAACTATCCTGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22096 CATGTGCTTCCTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ATTCCTGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATGCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 GCTAAGATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCA
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                                                                                                                                                                 Length 70836;
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; Pred. No. 2.1e-265;
0; Mismatches 0;
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larity 100.0%;
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Matches 936; (
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'S Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Banh, J., Bowner, L., Carninci, P., Chen, H., Yamamura, Y., Yu, G., Yuk, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Kosesma, E., Lam, B., Lin, J., Raylin-Neumann, G., Kawai, J., Kim, C., Kosesma, E., Lam, B., Lin, J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Direct Submission Standard, Capter, Gollection and Clustering of RaFi. cDNas (RaFi. cDNa.) RIKEN Genomic Sciences Center (GSC) members carried out the collection and Clustering of RaFi. cDNas (RaFi. cDNa.) 'RIKEN Arabidopsis Full-Length cDNa'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
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SM Arabidopsis thalians.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons;

Rosidae; eurosida II; Brassicales; Brassicaces; Arabidopsis.

S Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,

Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,

Arabidopsis Pull Length cDNA Clones

Unpublished

Unpublished

Unpublished
                                                                                                                                                                                                                                                                                                         AY063880 1341 bp mRNA linear PLN 25-APR-2002
Arabidopsis thaliana putative GDP-L-fucose synthetase (At1g17890)
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883 TCGAAGCTTGCGTCTTTGGGATGGACACCGAAGATTTCGCTTAAAGATGGCCTCTCCCAA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Location/Qualifiers
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/note="This clone is in a modified pBluescript vector
(Lambda ZAP) as a XhoI/SstI insert.
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HTG; HTGS PHASEI.

Arabidopsis thaliana.

SM Arabidopsis thaliana.

Spermatophyta; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosidae; turosida II; Brassicales; Brassicaceae; Arabidopsis.

Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,Q., Chin,C., Chlou,J., Choi,E., Conn,L., Conway,A., Gonzae,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaologis,A. and Ecker,J.R.

Genomic sequence for Arabidopsis thaliana BAC F20L2 from chromosome
                                                                                                      1029 TCGAAGCTTGCGTCTTTGGGATGGACACCGAAGATTTCGCTTAAAGATGGCCTCTCCCAA 1088
                                                                                                                                                                                                                                                                                                 AC025908 65262 bp DNA linear HTG 17-MAR-2000 Arabidopsis thaliana chromosome 1 clone F20L2, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-MAR-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 18th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                           969 GGAAAGCTTGTTTGGGATACCACAAAACCAGGAGGACACCAAGGAAACTGATGGATAGC
                                                                                 TCAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTTAGAGATGGTCTGAGCCAA
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gap of unknown length
6612: contig of 4083 bp in length
agap of unknown length
10394: contig of 3782 bp in length
gap of unknown length
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                                                          /product="putative GDP-L-fucose synthetase"
/protein id="AAL16236.1"
/br.xref=101:1738.04886.1"
/db xref=101:1738.04886888688FWLEKSAKIFVAGHRGLVGSAIVRKLQDQGF
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TNLVLRTHSELDLTSQSDVESFFATEKPVYULAAAKVGGHANNTYPADFIGVNLQI
                                                                                                                                                          OTNVIHSAYTHGVKKÜLFLGSSCIYPKPAPQPIPESALLTGFLEFTNEWYATAKIAĞI
KOQAYKLQHQMDAISOMPTINIKQONDRFPERBYULPALMRRHEKAKNNADEYVVW
GSGSPLREFLHYDDADACVELMDQYSGFEHVNVGSGVEVTIKELAELVKEVVGFKGK
LVWDTTKPDGTPRKLMDSSKLASLGWTPKISLKOGLSQTVEWYLENVVQKKQ.
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Pred. No. 3.1e-186;
0; Mismatches 162;
                                                                                                                                                                                                                                                                                  394
/gene="At1g17890"
/codon_start=1
/evidence=experimental
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                                                                                                                                                                                                                                                              /gene="At1g17890"
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Best Local Similarity 82.5%;
Matches 765; Conservative
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Direct Submission

L. Submitted (03-AUG-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, UBA

On Jul 29, 2000 this sequence version replaced gi:884119.

The sequence is of BAC F2H15 from Arabidopsis thaliana chromosome

1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 26271 bp because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future, for creation of larger contigs, we provide small overlaps (200 bp) between overlapping submitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone Fila6.

Fila6. The 3' end of this sequence overlaps by 200 bp to the 5' end of the sequence of the clone Fila6.
                                                                                                                                                                                                                                                                            Sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1,
                               8162 TCGAAGCTTGCGTCTTTGGGATGGACACCGAAGATTTCGCTTAAAGATGGCCTCTCCCAA 8103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; euroside II; Braesicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 7513)
Sakano, H., Liu, S.X., Etgu, P., Lee, J.M., Lenz, C., Pham, P., Toriumi, M., Yu, G., Chan, A., Chung, M., Goldsmith, A., Liu, A., Smith, A., Liu, A., Kan, S., Rushith, A., Vaysberg, M., Altafi, H., Brooks, S., Buehler, E., Chao, Q., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Sobthwick, A., Davis, R.W., Ecker, J.R., Federspiel, N.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Contains a DNA binding domain with preference for A/T rich regions PF|02178, a domain of unknown function PF|02182 and a SET domain PF|00856."
  841 TCAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of BAC F2H15 from Arabidopsis thaliana chromosome
Unpublished
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    75133
    /organism="Arabidopsis thaliana"
/cultivar="Columbia"

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5733. .5887,5980. .6177)
/gene="F2H15.1"
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/chromosome="1"
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Direct Submission
Submitted (04-APR-2000) Plant
Street, Albany, CA 94710, USA
3 (bases 1 to 75133)
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/gene="F2H15.1"
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGATCTCACTAGCCAATCAGATGTTGAATCTTTCTTTGCTACAGAGAAACCAGTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCATCCTAGCTGCTGCTAAAGTCGGTGGGATTCATGCTAACAACAACACATACCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9002 Argiradada Arcico de Argira de Contra de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATTGTCCGCAAGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGATCTCACTCGTCAAGCCGATGTTGAATCCTTCTTTTTCTCAAGAGAAGCCAGTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAATCCTAGCAGCAGCTAAAGTTGGTGGTATTCACGCTAACAACACCTATCCTGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCATTGGTGTCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8702 Greaagaacrecrecrecricerresrecrecerriraceceaarrirecrecreages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ATTCCTGAGTCTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGTGGTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 GCTAAGATCGCTGGGATTAAGACTTGTCAGGCTTATAGGATTCAGCACGGATGGGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGTGGGTTTGGGGAAGTGGAAGCCCGTTGAGGGAGTTTTTACATGTCGATGATTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGTCTGACAAATCTGCCAAAATCTTCGTCGCGGGTCATCGTGGTTTGGTTTGGATCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 AICTCTGGCATGCCTACTAATCTCTATGGTCCTAATGACAATTTCCACCCGGAGAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGTGCTTCCTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAA
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                                                                                                                                                                                                                                                                                                                                                          Length 65262;
                                                                                                                                                                                                                                                                                                                                                          Score 667.8; DB 2; Length
Pred. No. 5e-186;
0; Mismatches 162; Indels
55257: gap of unknown length
55257: contig of 6757 bp in length
gap of unknown length
65262: contig of 10005 bp in length.
                                                                                                                                1. .65262
/ Organism="Arabidopsis thaliana'
/db_xref="taxon:3702"
/chzomosomes="1"
                                                                                                                                                                                                                                                                            12081 g 19838
                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                /clone="F20L2"
12169 c 120
                                                                                                                                                                                                                                                                                                                                                       Query Match
71.3%;
Best Local Similarity 82.5%;
Matches 765; Conservative (
                         48501
                                                                             55258
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join(23881. .24264,24490. .24779,24869. .24959,25122. .25244,
25328. .23456,25595. .25738,25819. .25905,25987. .26259,
26348. .26455,26555. .26905)
/gene="F2H15.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Contains similarity to ATP dependent transmembrane transporter protein (wh3) from Bombyx mori gb|AF229609 and contains an ABC transporter PF|00005 domain. ESTB gb|Z18062, gb|AN59975, gb|N96732, gb|F14058, gb|AV528782, gb|AV55926, gb|AV556190, gb|AV562800, gb|AV559560, gb|AV523165, gb|AV56094, gb|AV56285 come from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not experimental
/protein id="AAF97264.1"
/db_xref="G1:9665062"
/translation="MBIBASRQTTVPVSVGGGNFPVGGLSPLSEAIWREKAPTEFVG
DVSARITWQDLTVWTWGDGFTQNVT.EGLTGYAEPGSLTALWGPSGSGKSTMLDALAS
RIAANAFLSGTVLLNGRKTKLSFGTAAYVTQDDNLIGTLITVRETIWYSARVRLPDKML
                                                                                                                                                                                                                                                                                                                    /protein id="AAF7762.1"
/db xref="GI:9665060"
/translation="MFSFVGFVVFLSGFFLGILAVLSAEAAGFMYLLKRLNRKRDRIE
                                                                                                                                                                                                                                                                                                                                                                                                                             SKPVSDPSIKDFNPRESIDFCINKQGVVWILELDEGLKNWMKEKLPKEQKRKRGLLEI
HPLRKFARIKDHKLILSDADSTQSETTVSLIGCSIBAVSGSDLPTRKWAKRFPIKVES
KISPALYKGNQVFYIYLETSWEKESWCKALRLASCENQERFIWYSTKLKEDFRNYVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAVAYPSFMKPSLGFSFETLDKGNRTDGSSSKVRLFLKKFSRKRSNREDRKTYSHHGS
SSGKCFPGKNNMTDDTDVPJFSRSVSHSSHIGGVSHLGGVSBCDSEEKVDMDEGTLAL
NLLISPLKRKTGVKNSVQARIQLSNWFTSYIGELICSDVDTGNLFPHIHAT
RVLPPRRAFGVWAFELDIEYSGDVVIDVETRVDIRGYGFITDTRLQPRSGVVVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAEGVEDFEKQLVFPVETVNAGEVKNDESKSSRGTKAAPNGVSRWKSILKTIAEQVSQ
VPISLSIRVSSLRGTLRVHMKPPPSDQLWFGFTSMPDIEFDLASSVGEHKITNSHVAM
FLINRFKTAIREAVVLPNCESLTIPWMIAEKDDWVQRKAAPFWMLNQENDHNTSHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARSKSDKPPTSFSCLQAEQMORTANATOKTISBIGTLASSSCAOSEOVOKAATAFOKO
NTEAEAIMSTPLSNSTTVTIENDKSLEELKTPLLVPSSSNKQETNSRGSSREVSAVQS
PSRSVASSEEDDSRGKKQGRRARMLDLGKKMGEKLEEKRRHMEEKSRQIVEKMRGPS"
complement (17129. .19183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MVGERMWWWSSSTKLRSNLERFLRGITPKPPSFSLSQSCKNDL
NSRMHHENGESTRYPRLSDLMOFCPBEAYGHGSKVDLMNGESVMQTVPYLSATQIY
TNKSTAISRTHSDVUDCESEGWSDDSEIEKLSRSMSSGSSKTWDSVSDDSGYEIDGTS
SLMRDKLGSIDPQYFESVKPHLRVPLTAKVNELAEKYPGLSTLRSVDLSPASWLAIAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIPLAPFGLVSYKLQGDLWRNQECGDQGRIVYLRSAADSWLKQLNVQDHHDHSFFSMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(17129. .17397,17526. .17617,17707. .17792,
17894. .18128,18214. .18431,19070. .19183))
/gene="F2H15.6"
                            compiement(join(12762. 13436,13526. 13720,13893. 13987
14151. 14499,14602. 15232,15319. 15560,15920. 16126))
/gene="£2H15.5"
                                                                                                                                                          /note="Strong similarity to a hypothetical protein IRK17.13 g1|6598861 from Arabidopsis thaliana BAC T18K17 gb|AC010556 and contains a PH PF|00169 domain." | codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Strong similarity to a hypothetical protein T18K17.12 gi|6598871 from Arabidopsis thaliana BAC T18K17 gb|AC010556. EST gb|A1996552 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Pred. No. 5.1e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/protein_id="AAF97263.1"
/db_xref="GI:9665061"
                                                                                                                                                                                                                                                                                               experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F2H15.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="F2H15.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon start=1
                                                                                                                                                                                                                                                                                               /evidence=not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23881. .26905
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82.5%;
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Best Local Si
Matches 765;
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GDDGWDPVVPMDTWARGKTFYAGDILEFKYDYQRFNLIVVNRTGYETCEANVGAIEYS
SGDDKIQLNYGYNYFIGTYTPEDCTTGLKMAIKALAPR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MATSARRAYGFGRADBATHPDSIRATLAEFLSTFVFVFAGEGSI
LALDELYWDTAAHTGTNYTPGGLVLVALAHALALFRAYSAAINVSGGHVNPAYTFAALI
GGRISVIRAIYYWYQLIGATLACLLIRLATNGLRPVGFHVASGVSELHGLLMEIILT
FALVYVYYSTAIDPFRGSIGIIAPLAIGLIVGANIILVGGPFDGASMNPARAFGPALVG
WRWSNHWIXWVGPFIGGALAALIYEYMIIPSVNEPPHHSTHQPLAPEDY"
                                                                                                                                                   TSPLLMVPPLRTIWPSNXEWYDGDAGPSSTGPIKREASDNTNDTAHNTFAPPPEMNIP
LITIREDSDSNYSCDAGAGPSTGPYKRGRGRFKGSKNSTPTBFKKYKYDVBUSLKVT
SLGTIRDSETTEASTEGNOEI USVWMRFDARRELOGINHPEDILTTASGNCTROGY
KTNTRRRIGAVPGIHVGDIFYYWGEMCLVGLHKSNYGGIDFFTAAESAVBGHAAMCVV
                                                                                                                                                                                                                                                                                        TAGQYDGETEGLDTLIYSGQGGTDYYGNARDQEMKGGNLALEASVSKGNDVRVYRGYI
HPHENNQKIYIYDGMYLVSKFWTVTGKSGFKEFRFKLVRKPNQPPAYAIWKTVENLRN
HDLIDSRQGFILEDLSFGAELLRVPLVNEVDEDDKTIPEDFDYIPSQCHSGMMTHEFH
                                                                                                                                                                                                                                                                                                                                                                                          FDRGSLGGONCRHQPCMHQNCTCVQRNGDLLPYHNNILVCRKPLIYECGGSCPCPDHC
TRIVYQTGALLHLEVPKTRNCGMGIRSMDPIRAGTFICEFAGLIKTKREBYBEDDDYLF
DTSKI YQRFRWYYBEBLLLEDSWEQVSEFINLPTQVLISAKEKGNVGRFMHSCSPNV
FWQPIEYENRGDVYLLIGLFAMKHIPPMTELTYDYGVSCVERSBEDGGFLVCPYLISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWPSSSEIHFLINSKGRAWYDKIYRKLASQGNVSSGLDSVKDEPEKLREEQMEGDGFK
EKLSDSVLIDEKLEEYSDCDRTATTSRSHTDPVSSQSTHQTPESFRTPITCDDDTFVS
VSGISRDVSNLIPFATETPASPVQEKMANTRSFSNNSVKGNQDEFFIEDFDVGPMDTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLYDMTFREDPSDFDDNLLYAMRDRTKQLRSFKRKIMDAIKSKRRREKEYEQLAIWFG
DADMGCDLVNDKEQSTTSIDSKSSQTNVPVVSEDSEWEIL"
COMPLEMENT (6878. .8287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein id="ACP97259.1"
/db_xref="G1:9665057"
/translation="MSSEHISGGGASKTKKHKWSSSQNRPKPMGVSRQERSVPLVSPS
NSFASEDDHHMLKISLSSISKLEVRNLKRKLKSELDEVRSLIKRFDPEANPGGSMAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVVGRSKKVKTGNGGGKKSGHCADKGTVQI FKNCNSLLTKLMKHKSAWVFNVPVDAKG
LGLHDYHNIVKEPMDLGTVKTKLGKSLYKSPLDFAEDVRLITFNAILYNPIGHDVYRP
AELLLANNFEDKWVS IEMQYDNLHRKFKPTRDI EFPAPAPSI TATVEPLPAI VESPSPS
SPPPPPPPVAAPVLENTWEREESWTI PVYEBAAVI TAPEKAEEEEAPVNNRDLJTLEE
KRRLSEELQDLPYDKLETVVQI IKKSNPELSQKDDEI ELDIDSLDINTIWELYRFVTG
YKESLSKKNEAHGFGSERDAESVHNSI QEPTTLVSGTTTSRVTESGKL"
                                                                                                                          translation="MDKSIPIKAIPVACVRPDLVDDVTKNTSTIPTMVSPVLTNMPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Contains similarity to blue copper-binding protein
III from Arabidopsis thaliana gb|U65650 and contains a
Plastocyanin-like PF|02298 domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Identical to beta-tonoplast intrinsic protein (beta-TIP) from Arabidopsis thaliana gb|AF026275 and contains a MIP (major intrinsic protein) PF|00230 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Contains similarity to female sterile
homeotic-related protein Frg-1 from Mus musculus
gb|AF045462 and contains a bromodomain PF|00439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(11220. .11361,11662. .11927,12058. .12453)
gene="F2H15.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join(6878. .6934,7022. .8287))
/gene="F2H15.2"
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/gene="FR115.3"
join (9839. .10049,10191. .10402)
/gene="F2H15.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="Similar to LINE element"
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/protein_id="AAF97260.1"
/db_xref="G1:9665058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               experimental
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                     /evidence=not_experiment:
/protein_id="AAF97258.1"
/db_xref="G1:9665056"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F2H15.2"
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/evidence=not_e
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120 240 300 498 GAACACATTCCGAG 318 AGAAGCCAGTTTAT 180 438 9 AAACACACGCCGAG CCTATCCTGCTGAT CATACCCAGCTGAT TTCATTGGTGTCAAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGT TTCATTGGTGTCATCTCCCAAATTCCAGACCAATGTGATCCACTCTGCTTATAAGCACGGT TGGTTGGATCTGCC 1; Gaps 241 439

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RESULT 8
AY089031
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY089031 1353 bp mRNA linear PLN 21-JUN-2002 Arabidopsis thaliana clone 19576 mRNA, complete sequence.
AY089031.
FLI CDNA.
thalla cress.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; core eudicots;

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CAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGCCCAAA 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22747 TCCCGGAGAACTCCCTCCTCTCCGGCCCCCTCGAGCCCAACGAGGTGGTACGCCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAGATCGCCGGAATCAAGATGTGCCAGGCTTACCGCATCCAGCACGCCTTCGACGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22867 TCTCGGCCATGCCCACCACCTCTACGCCCCGCAGACATCCACCTCCACCCGGAGAATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGCGAGGTGACGATCAAGGAGGTCGCGGAGCTGGTGAAGGAGGTGGGTTGGGTTCCAGG
                                                                                                                                                                                                                                                                                                               65 TCCGCAAGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTCACTCGTCAAGCCGATGTTGAATCCTTCTTTTCTCAAGAGAAGCCAGTTTATGTAA
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                                                                                 (japonica cultivar-group)
      and
                                                                                                                                                                                                                                      Length 130393;
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    soon as it is available
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                                                                                                                                                                                                                                  Score 430.6; DB 2;
Pred. No. 8.6e-116;
0; Mismatches 299;
                        be preserved
                                                                                                                                                                              38530
                                                                            /organism="Oryza sativa
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
                                                                                                                                                   /clone="OSJNBa0085J13"
26888 c 27585 g 38
    the finished sequence as
by the finished scar-
the accession number will b
Location/Qualifiers
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 67.4%;
Matches 623; Conservative
                                                        1. .130393
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E (bases 1 to 130393)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
L Submitted (02-MXY-2001) Takuji Sasaki, National Institute of Direct Submission
L Submitted (02-MXY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 30-8602, Japan
(E-mail: tsasakiabar.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-299-38-7469)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a vailable and the accession number will be preserved.
* NOTE: This is a "working daraft' sequence.
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                ATCTCCGGTATGCCCACGAATCTGTATGGTCAGAATGATAATTTCCACCCGGAGAATTCC
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:OSJNBa0085J13
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Archaea Euryarchaeota; Methanosarchnales;
Methanosarchaceae; Methanosarchaea;
I (bases 1 to 10029)
S Deppenmeier, U., Johann, A., Hartsch, T., Merkl, R., Schmitz, R.A.,
Martinez-Arias, R., Henne, A., Wiezer, A., Baeumer, S., Jacobi, C.,
Brueggemann, H., Lienard, T., Christenann, A., Boemecke, M., Steckel, S.,
Bhattacharyya, A., Lykidis, A., Overbeek, R., Klenk, H.-P.,
Gunsalus, R.P., Fritz, H.-J. and Gottschalk, G.
The genome of Methanosarcha mazai Evidence for lateral gene
transfer between Bacteria and Archaea

IL J. Mol. Microbiol. Biotechnol. (2002) In press
2 (bases 1 to 10029)
Brueggemann, H., Lienard, T., Christenan, A., Boemecke, M., Steckel, S.,
Brueggemann, H., Lienard, T., Christenan, A., Boemecke, M., Steckel, S.,
Brutacharya, A., Lykidis, A., Overbeek, R., Klenk, H.-P.,
Gunsalus, R.P., Fritz, H.-J. and Gottschalk, G.
Direct Submission

Li Direct Submission
Submitted (23-AUG:201) Goettingen Genomics Laboratory, Institute
for Microbiology and Genetics, Grisebachstrasse 8, Goettingen
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Archaea; Buryarchaeota; Methanococci; Methanosarcinales;
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Physicomitrella patens

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;

Bryopsida; Funarilae; Funariales; Funariaceae; Physicomitrella.

Bryopsida; Funariales; Funariales; Funariaceae; Physicomitrella.

Lerchl, J., Renz, A., Ehrhardt, T., Reindl, A., Cirpus, P., Bischoff, F., Frank, M., Freund, A., Duwenig, B., Schmidt, R.M. and Reski, R.

Mass genes from physicomitrella patens encoding proteins involved in the synthesis of carbohydrates

Patent: WO 0144476-A 147 21-JUN-2001;

BASF Plant Science GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEATVFLLONYSAHEHVNMGSGSEVSIKELAEMVKEVVGFOGOLTWDTSKPDGTPRKL
IDSSKLANMGWQARIPLKEGLAETYKMYCENYNV"
308 c 410 g 402 t 1 others
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                                                                                                                                                                                 Sequence 147 from Patent W00144476. AX172657 AX172657.1 GI:14597769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MyPKQFLKFGETSLFQETVLRCLEVSDISEVFVVTNEAQKFFVI
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                                                                                                                                                                                                                                  GENLQWLLYLNPLTGLISAHRACLLGHIPVDFVGLGISAVLTVVIFVSGILYLRSTEK
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                                                                                                                                                                                                                                                                                                              complement (4788. .5726)
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HRSRSRLILKGFQQEKKFSWDKTASETFNVYKSIIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="Polysaccharide ABC transporter, ATP-binding
                                                                                                                                                                                                                                                                                                                                                                             /product="glycosyltransferase involved in cell wall
biogenesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Polysaccharide ABC transporter, permease protein"
   'organism="Methanosarcina mazei Goel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein_id="AAM30350.1"
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                                                                       db_xref="taxon:192952"
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                                                                                                                                                                                          complement (157. .903)
                                                                                                                                                                                                                                                              /EC_number="2,4,-,-"
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trans1 table=11
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                                                                                                                                                   'gene="MM0653"
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Clostridium acetobutylicum ATCC824 section 206 of 356 of the complete genome.
AE007718 AE001437
AE007718.1 GI:15025171
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Childress, D., Zeng, Q. and Smith, D.R.
Direct Submission
Submitsed (24-JUJ-2001) GTC Sequencing Center Production,
Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Waltham, MA 02453-8443, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon start=1
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INLNLSNSHLDAPQQIKGRNFEVPACGAFILTSDVGGLSHYYEIGKEVVVYSSFDDM
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FRYKEKADVLSVIFKNAVGKNIGIYGSGDHTTNLIKYYKKLIGDIKFNTYYFDSNSL
KWGTBYLGGIIHSPKEIDELNLDRIIISSYEYEEDIFKYLNEITSGINIVKIYNGDKK
ENLFTD"
                                                                                                                                                                                             4883 ATTACAAAATTGAGCTCACTTGGGTGGAAAGCTAATATCTCATTAAAAGATGGAATTAGA 4824
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Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q.,
Gibson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I.,
Tatuson,R.L., Sabathe,F., Doucette-Camm,L., Soucaille,P.,
Daly,M.J., Bennett,G.N., Koonin,E.V. and Smith,D.R.
Genome sequence and comparative analysis of the solvent-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                             778 GAAGGGAAGCTTGGATGGGATTGCACTAAGCCAGATGGCACACCGAGGAAACTTATGGAC
                                                                                  4943 AAAGGTGAAATTAGAAAGATCTTTCAAAGCCTGACGGTACTCCACAGAAGCTGCTTGAT
                                                                                                                                              838 AGCTCAAAGCTCGCGTCTTTGGGTTGGACACCTAAGGTTTCTCTTAGAGATGGTCTGAGC
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/Brrain="ATCC 824"
/db_xref="ATCC 824"
/db_xref="taxon:1488"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterium Clostridium acetobutylicum
J. Bacteriol. 183 (16), 4823-4838 (2001)
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/gene="CAC2177"
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/gene="CAC2177"
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/transI_table=11
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FSVEI LAEDPDI SKSQYKGLPVESLKLKAWV"
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MLIKDDNEKLVKRFNLPKKKVCFHPKPKMKYKSVAFFPRYIWRCINYAARTSNNSNLE
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LQVDDEGDVYSCDIPKGSLGSGDNKIIINFNHNASPEEAKNDWERRKKRINKRILFIK
MTLPANNEELVKRFDNLPYKNKVCFYPRPMKYKSIVFCPRYIWKCKNMARKTSNYDLV
                                                                                                                                                                                                                                                                                              /trānslation="mykCLIWGVSDEYTMAYDKLLFEILKKNLSIEALISKDKYAEYI
DGKKVIDKTEISNYQFDYIIIFNKERYSDIKNEALELGIPERKILNGKVFFTSNFDFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3390 TACTATTTTAGGGAGTTCTTGTATATATCCTAAAGAAGCACCACAGCCTTTGAAAGAAG 3331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 TCAATCTCCAGATTCAGACCAATGTGATCCACTCTGCATATGAGCACGGTGTGAAGAAGC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTTTGTTAACAGCATCGCTTGAACCAACTAATGAGGTGTTATGCTATTGCTAAGATCG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 TGCCTACTAATCTCTATGGTCCTAATGACAATTTCCACCCGGAGAATTCTCATGTGCTTC 550
                                                                                                                                                                                        protein, homolog HI1244 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein, homolog HI1244 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3570 TGCACCAAGAAAGTTATAAGAAGTTCCTTGAAGAAAAGAAAAGCCTGATTATGTAGTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3690 AAGATAGCAAAATATATATATAGCAGGTCATACTGGTTTTTGTTGGTTCTGCCATATTAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3630 ATTTAGAGCGTAGAGGATATAAAAATGTTGTAGTGAGAACTCATAAAGAACTTGATTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGTCAAGCCGATGTTGAATCCTTCTTTTCTCAAGAGAGCCAGTTTATGTAATCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3510 CAGCTGCAAAGGTTGGTGGAATACAAGCGAATATTTCGAATCCTGTGGACTTTCTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3450 ATAACCTAATAATAGAATATAATGTGATAAAAAATTCTTTTGAGGTAGGAATTGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCTTCCTTGGATCATCCTGCATTTACCCTAAATTTGCTCCTCAGCCAATTCCTGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGGCTAAAGATGTGCGAATATTATAGTAAGCAGTATGGATTAAATTACATAAGTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTTCAGGAACAAGGTTTCACCAATCTCGTTCTTAAAACACACGCCGAGCTTGATCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 301.8; DB 1;
Pred. No. 8.1e-78;
0; Mismatches 377;
                                                                                                                                                                                                                                                                                                                                                                                                                             YFVMDTNWLQKSCDILKMLCGEDDFIREK"
                                                                                                                                                                                        product="Uncharacterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Uncharacterized
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                                                                                                                                                                                                              Haemophilus influenzae"
/protein_id="AAK80142.1"
/db_xref="GI:15025179"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         7463. .8380
/gene="CAC2185"
7463. .8380
                                 ;136. .7053
/gene="CAC2184"
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/gene="CAC2185"
                                                                                                           /gene="CAC2184"
        MDPNRGNNIDIRV"
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32.2%;
Best Local Similarity 58.7%;
Matches 541; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1429 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKEDSKIYIAGHTGFVGSAILRNLERRGYKNVVVRTHKELDLMH
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LIFLGSSCITYPKEAPQPLKEEYLLSGYLEPTNRGYAAAKISGLKMCERYSKQYGLNYI
SAMBSNLYGYRRDNPICKTSHYMAALIRRFHEAKVSGSQEISINGSGEGYREFTYIEDL
ADGIIFLMEHGEKVKGFLNIGGGKDIKIKDLYGLYKTUVGFKGNIIFDKSKFDGMFRK
VMDVSKINSLGMHYKVELDEGIIKTYRWYLNNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKKAIITGITGQDGSYLTEFLLKKGYEVHGIIRRASSFNTKRID YLEDPKIGNKLLFLHHGDLTDSSNINRLLEKYQPTEIYNLAAQSHVOYSFVPEYTV ETDAVGTLRFLDAIKELGIKKKFYQASTSELFGGMFGTAPQSEKTPFYPRSPYAAAKL YAWITVNYRBAYGIPACNGVLFNHESPRAGETFVTRKITRALANIIEGNQDKVSLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNAKRDWGYAGDYVZAMWLMLQKDTPKDYVIATGETHTVREFVEKAFKFAĞIKIKWIG
QGIEEKGIDLKTGKTLVDVNPRYFRPTEVELLLGDPSMAERELGWRRKVNFEELVYMM
VEEDLKKTRITNVDRVRELLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mmrlcrlyitutilenkilelekiedrfeklirdkkdilyydrf
fnvilsesdreyacnydytynllkstwypvfkskinmingklggyknyknk"
                                                                                                        QGCKYSVFVNSGSSANLVLLSAVKDYYNLDNTSEVIVPAVTWYNISPILQCGLKPVF
VDVNLEDLSFDYEELKKKITDKTKAIFITHLLGFPANMEKIKNVIGEKDIVILEDCCE
                                                                                                                                                             SHGAKYKNI KVGNFGLGGTFSFYWGHHMTTI EGGMI STNNEEFYKLCLLKRSHGLARE
                                                                                                                                                                                   LPIKYHEYYKNKYKDIDFKFLFLTDGFNVRSTEINAFLGLRQIKNLDAFIEIRDKNYN
MFFDTCTKYEDKLITIKVEGTSSLALPFIFKEKRLREIVEKKLNELGVETRPIISGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDIALLATINSNEKVNEAANLAVFKMAMNCKQNGENTADMIEA
                                                                                  translation="MKWKLQENALVKEEIESLAEFIKTADRLTQGSKVKEFEAEWSKW/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNIKFLLVCMCIMVKAYKVCYRINYQANISELESFYIR" complement (5827. .6000)
                                                                                                                                                                                                                                          LRQPFLKKYHNENEFKNANLIHDNGFYIGNNQFVDEIRLKKLESILDKIM"
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Nucleoside-diphosphate-sugar epimerase"
CDP-4-keto-6-deoxy-D-glucose-3-dehydrase"
/protein_id="AAK80136.1"
/db_xref="G1:15025173"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein id="AAK80139.1"
/db_xref="G1:15025176"
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/product="Hypothetical protein"
/protein id="AAK80140.1"
/db_xref="G1:15025177"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAK80137.1"
/db_xref="GI:15025174"
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/db_xref="GI:15025175"
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/db_xref="GI:15025178"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (5047. .5334)
/gene="CAC2181"
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/gene="CAC2183"
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/gene="CAC2180"
                                                                                                                                                                                                                                                                   complement (2768. .3697)
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                                                                                                                                                                                                                                                                                                                    .3697)
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/product="Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (5386. .5502)
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                                                                                                                                                                                                                                                                                                                       complement (2768.
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                /gene="CAC2179"
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                                                                                                                                                                                                                                                                                         /gene="CAC2179
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/trans1_table=
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGATGGAACCCCGCGCAAACTATTGGACGTCTCCGCGCTACGCGAGTTGGGTTGGCGCC 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gsbA gene; gsbB gene; gsc gene; gsd gene.
Mycobacterium avium subsp. paratuberculosis.
Mycobacterium avium subsp. paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                              TCGCGGGTCATCGTGGTTGGTTGGATCTGCCATTGTCCGCAAGCTTCAGGAACAAGGTT
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                                                                                                                                       224 TIGATTTIGIGICIGAGACAAGACCACAGGIGATCATCGATGCGGCCGCCACGGGTCGGCG
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Hermon-Taylor,J., Doran,T., Millar,D., Tizard,M., Loughlin,M., Sumar,N. and Pord,J.
NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES IN PATHOGENIC MYCOBACTES AND THEIR USE AS DIAGNOSTICS, VACCINES AND TARGETS FOR CHEMOTHI PREDEI: WO 9723624-A 15 03-JUL-1997;
ST GEORGE S HOSPITHAL MEDICAL S (GB)
Other publication AU 1202797 19970717.
                                                                 CTGCTCTTATGAGGAGGTTCCACGAGGCGAAAGTGAATGGAGCGGAGGAAGTTGTGGTGT
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    Thote="unnamed protein product; Protein sequence is conflict with the conceptual translation" /codon_start=1

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TYTGMSGIRLLEAVULSPYNCRFYQASSBWFGASPPPVTRSTPFYRRYFS
YWTTRNYREAYQLFAYNGILIRHESPRRGFTFVTRKITRAVARIRAVGSBYYMGNLD
AIRDWGYAPEYVEGMWRMLQAPEPDDYVLATGRGYTVREFAQAAFDHVGLDWQKHVKF
MLDGWGGYAPEYDSLVGDADRAAQSLGWKASVHTGELARIMVDADIAASECDGTFWIDTP
MLDGWGGYS".
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ANGOFGSALRRAGFKSRIVSFEPLGGFFAQLTRESASDPLWECHQYALGDADETITI
NVAGNAGASSSVLPMLKSHQDAFPPANYIGTEDVAIHRLDSVASEFLNPTDVTFLKID
VQGFBRQVIAGSKSTLNBSCVGWQLELSFIPLYBGDMLIHEALBLUYSLGFRLTGLLP
GFTDPRNGRMLQADGIFFRGDD"
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/db_xref="G1:3550478"

/db_xref="SPTREMBL:086292"

/translation="WRRALITGITGODGSYLAELLLSKGYEVHGLVRRASTFNTSRID
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/db_xref="Eq:13550476.29"
/db_xref="SPPREMB1:086293"
/translation="MRWHTMDRHADVAWLGRSKLTTTPGPLDRATPVYIAGHRGLVGS
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PADFLSENIRIQTNLLDAAVAVRVPRLLFLGSSCIYPRYAPOPIHESALLTGPLEPTN
DAYAIAKIIAGILQVQAVRRQYGLAMISARPTNLYGPGDNFSSBGSHLLPALIRRYSEA
KAGGAEEVTNWGTGFPRELLHYDDIASACIFLIEHPOCPNHYNVGTGVDHSISEIDA
WVATAVGYIGETRWDPTKPDGTPRKLLDVSALRELGWRPRIALKDGIDATVSWYRTNA
                                                                                                                                                                                    2 (bases 1 to 4435)
Tizard,M., Bull,T., Millar,D., Doran,T., Martin,H., Sumar,N., Ford,J. and Hermon-Taylor,J.
A low G+C content genetic island in Mycobacterium avium subsp. paratuberculosis and M. avium subsp. silvaticum with homologous genes in Mycobacterium tuberculosis
Microbiology 144 (Pt 12), 3413-3423 (1998)
99099703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mycobacterium avium subsp. paratuberculosis"
|sub species="subsp. paratuberculosis"
|db_xref="taxon:1770"
201. .1232
                                                                                        Direct Submission
Submitted (29-JNN-1998) Bull T., Surgery, St Georges Hospital
Medical School, Cranmer Terrace, London, SW17 ORE, UK
2 (bases 1 to 4435)
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/protein_id="CAA11577.1"
/db_xref="G1:3550480"
/db_xref="SPTREMBL:086294"
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201. .1232
/gene="gsbA"
/function="unknown"
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/gene="gsbB"
/function="unknown"
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1172. .2101
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3335. .4135
/gene="gsd"
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/gene="gsc"
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AND TARGETS FOR CHEMOTHERAPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGCATTTACCCTAAATTTGCTCCTCAGCCAATTCCTGAGTCTGCTTTGTTAACAGCAT 388
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Hermon-Taylor, J., Doran, T., Millar, D., Tizard, M., Loughlin, M., Sumar, N. and Pord, J.
NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES IN PATHOGENIC MYCOBACTEI AND THEIR USE AS DIAGNOSTICS, VACCINES AND TARGETS FOR CHEMOTH: WO 9732624-A 4 03-JUL-1997,
ST GEORGE S HOSPITAL MEDICAL S (98)
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SUMMARIES

		Description	Sequence 2, Appli	Sequence 148, App	Sequence 4, Appli	Sequence 16, Appl	Sequence 6, Appli	Sequence 3862, Ap	Sequence 7, Appli	Sequence 260, App	Sequence 260, App		Sequence 260, App	Sequence 260, App	Ĺ	Sequence 260, App	Sequence 240, App	Sequence 260, App	Sequence 260, App		Sequence 260, App
		ID	US-09-318-271-2	US-09-734-569-148	US-09-318-271-4	US-09-734-569-16	US-09-318-271-6	US-09-738-626-3862	US-10-168-066-7	US-10-028-072-260	US-10-121-049-260	US-10-123-904-260	US-10-140-470-260	US-10-175-746-260	US-10-176-918-260	US-10-176-921-260	US-10-227-884-240	US-10-137-865-260	US-10-140-474-260	US-10-142-431-260	US-10-143-114-260
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                                                                                                                  APPLICANT: Running, Jeffrey A.
APPLICANT: Severson, David K.
APPLICANT: Buritingame, Richard P.
TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"
FILE REFERENCE: 3161-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 321;
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                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/318,271A
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 60/125,073
EARLIER FILING DATE: 1999-03-17
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 60/125,054
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1998-06-08
EARLIER FILING DATE: 1998-06-08
                                     Sequence 4, Application US/09318271A
Patent No. US20020012979A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09734569
Patent No. US20020064816A1
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Schmidt, Ralf-Michael
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SEQ ID NO 4
LENGTH: 321
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Best Local Similarity 56.9°
Matches 177; Conservative
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Reindl, Andreas
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US-09-318-271-4
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APPLICANT: Renz, Andreas
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                                     180 HVLPALMRRFHEAKVN-----WSGGSCGVGYKVVPLEGKFLHVDDLADACVFLLDRIQ 232
                                                                              290
                                                                                                     233 RGLEHVNIGSGQEVTIRELAELVKEVVGFBGKLGWDCTKPDGTPRKLMDSSKLASLGWTP 292
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SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1
SEQ ID NO 148
LENGTH: 310
HVLPALMRRFHEAKVNGAEEVVVWGTGS
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                                                                                                                                                       291 KVSLRDGLSQTYDWYLKNVCNR 312
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Schmidt, Ralf-Michael
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ORGANISM: Physcomitrella patens
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rank, Markus
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                                                                                                                                                                                                                                                                                                                                                                              Renz, Andreas
Ehrhardt, Thomas
Reindl, Andreas
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APPLICANT: Renz, Andres
APPLICANT: Ehrhardt, Th
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Best Local Similarity
Matches 231; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                          845702 seqs, 674182571 residues
                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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936
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Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:* /cgn2 6/prodate/2/pubpna/USO9_PUBCOMB.seq. /cgn2 6/prodate/2/pubpna/USO0 PUBCOMB.seq. /cgn2 6/prodate/2/pubpna/US10 PUBCOMB.seq. /cgn2 6/prodate/2/pubpna/US10_PUBCOMB.seq. /cgn2 6/prodata/2/pubpna/US60_PUBCOMB.seq. Published Applications_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		pli	App	pp1	4pp	oli	Appli	4pp1	ppli	ppli	, Ap	App	App	App	App	App	, Ap	, Ap	App	App
	u	e 1, A	e 147,	49, AI	121, 1	1, Apj	e 3, Ag	e 15, 1	e 2, App]	e 5, A	e 2058	296,	e 296,				e 1521	e 1521		
	Description	Sequence 1, Appli	Sequence 147,	Sequence 49, App]	Sequence 121, App	Sequence 1, Appl	Sequence 3,	Sequence 15	Seguence 2,	Sequence 5, App]	Sequence 2058,	Sequence 296,	Sequence 296	Sequence 296	Sequence 253,	Sequenc	Sequence	Sequence 1521	Sequence 190	Sequence 156
		71-1	59-147	1-49	0-121	4-1	71-3	59-15	05-2	71-5	93B-2058	0-296	17-296	63-296	43-253	45-638	00A-1521	28-1521	2A-190	4-156
	۵	US-09-318-271-1	US-09-734-569-147	5-09-894-84	S-10-114-17	US-09-939-964-1	US-09-318-271-3	US-09-734-569-15	US-09-962-805-2	US-09-318-2	US-09-294-093B-2058	JS-10-025-380-296	US-09-922-217-296	US-09-833-263-296	US-09-815-343-253	US-09-770-445-638	US-09-920-300A-1521	US-10-033-528-1521	JS-09-938-842A-190	JS-10-184-644-156
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	Query Match Length DB	1583	1490	996	14187	536165	996	701	933	1340	282	447	447	447	929	846	492	492	1332	413
, de	Query Match	91.6	41.8	29.4	28.8	28.3	28.0	22.8	15.6	10.9	6.4	6.3	6.3	6.3	4.8	4.7	4.1	4.1	4.1	4.1
	Score	857	391	275.2	269.8	265	262.2	213.6	145.8	101.6	59.8	58.8	58.8	58.8	44.8	43.8	38.6	38.6	38.4	38
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Sequence 156, App	٠,		Sequence 154, App	Sequence 98, Appl	Sequence 96, Appl	Sequence 7, Appli	Sequence 60, Appl		à	Seguence 346, App		6231	Ι,	ο,	ά,	Sequence 259, App	٠ م		259,	٠.		259,	259,	259,	250	1
9 US-10-184-634-156	9 US-09-735-056-1	9 US-09-918-995-26997	9 US-10-097-340-154	9 US-10-171-311-98	9 US-10-171-311-96	12 US-10-044-090-7	Ĭ.	9 US-09-796-692-8082		9 US-10-184-644-346	9 US-10-184-634-346	10 US-09-815-242-6231	₽	9 US-10-028-072-259	ns-	9 US-10-123-904-259	9 US-10-140-470-259	9 US-10-175-746-259	9 US-10-176-918-259	9 US-10-176-921-259	9 US-10-227-884-239	9 US-10-137-865-259	9 US-10-140-474-259	9 US-10-142-431-259	030 811 681 01 011	9 05-10-143-114-233
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38	36.6	36.4	36	36	36	36	35.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8			44		24.0		4. 8 8. 8
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ALIGNMENTS

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APPLICANT: Berry, Alan
APPLICANT: Berry, Alan
APPLICANT: Running, Jeffrey A.
APPLICANT: Running, Jeffrey A.
APPLICANT: Burlingame, Richard P.
ITILE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"
FILE REPERENCE: 3161-24
CURRENT APPLICATION NUMBER: US/09/318,271A
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 60/125,073
EARLIER PILING DATE: 1999-03-17
EARLIER PILING DATE: 1999-03-18
EARLIER PILING DATE: 1999-03-18
EARLIER PILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver: 2.0
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Pred. No. 2.8e-274;
0; Mismatches 15;
Sequence 1, Application US/09318271A Patent No. US20020012979A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.6%;
97.1%;
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Best Local Similarity 97.1
Matches 918; Conservative
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; LOCATION: (49)..(990)
US-09-318-271-1
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encoding proteins involved
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      Physcomitrella patens
s of carbohydrates
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Pred. No. 3.6e-119;
0; Mismatches 315;
TITLE OF INVENTION: Moss genes from Physcomitry TITLE OF INVENTION: in the synthesis of carbo FILE OF INVENTION: in the synthesis of carbo GURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16

NUMBER OF SEQ ID NOS: 181

SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1

SEQ ID NO 184
                                                                                                                                                                                                                                              ; LOCATION: (347)..(1276)
; OTHER INFORMATION: c_pp001064043r
US-09-734-569-147
                                                                                                                                                                              TYPE: DNA ORGANISM: Physcomitrella patens
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Best Local Similarity 65.0%;
Matches 596; Conservative
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LOCATION: (34)
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Fatent No. US/0020064816A1
GENERAL INFORMATION:
APPLICANT: Lerchl, Jens
APPLICANT: Renz, Andreas
APPLICANT: Reindl, Andreas
APPLICANT: Cirpus, Petra
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Frank, Markus
Freund, Annette
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